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(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a

5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays

10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for

15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to

20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- 10 Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment
- 15 of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the
- 20 Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- 25 Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).
- As used herein, the term primer refers to a single-
- 30 stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. -The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

- 5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
- 10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
- 15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
- 20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

- The direct analysis of the sequence of polymorphisms of
- 25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
- 30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be

- 5 identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in

- 15 electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary
20 structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(\text{AA}) = x^2$
 Homozygote: $p(\text{BB}) = y^2 = (1-x)^2$
 Single Heterozygote: $p(\text{AB}) = p(\text{BA}) = xy = x(1-x)$
 Both Heterozygotes: $p(\text{AB}+\text{BA}) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(\text{ID}) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(\text{ID})$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25 $p(\text{ID}) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(\text{ID})$ and $p(\text{exc})$.

The cumulative probability of identity ($\text{cum } p(\text{ID})$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30 $\text{cum } p(\text{ID}) = p(\text{ID1})p(\text{ID2})p(\text{ID3}) \dots p(\text{IDn})$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- The probability of parentage exclusion (representing
30 the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3})\dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified.

Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ), ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, supra. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, 5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is 10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene 15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating 20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15

EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different reference sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined a priori, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAACTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGTCT
						GAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT
						GTA CTGGCCAAATACTGAATAAACAGTTGAAGGAAGACATTGGAAAAAGCTTTTGAGGATAATGT
WI-7070	226	CT	---		---	TACTAGACTTTATGCCATGGTGCTTTTC/TAGTTTAACTGCTGTCTCTGTCTG
						AAGCCATTGACGTAACATCTCAGAGGTTATTTGTCATGGATTGACTCTGGGACAAAAGGAC/GC/AA
						AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTTT
						GATAATACATAAGCCCCCTAGGATTTAGATACAATCTTGAAAGAAACTGAGACAGATAATCTGAAAT
WI-10744	61	GC	---		---	AAATGAGGTAAAGTTTCAGGCATCA
						GGCAAAATTACCAGCAAAAGTCAAAATTACCAGCATCAAAGTCAGGTGCAAAAGGAGGTAGAACAA
						TTACAGTAACATATGTCAATCTTTTGTATATTAGTATTATCTGCCCAATGCCCTAGAATA/C/TJAGTG
						GGTCCCTAATAGTTATTAGTCCCTTTTCTCCTCTTCTCAATCTCTGAAATTTATTTTATACTTAA
WI-9975	126	CT	---		---	GGGATTAGTTACCACCAAAATGTGTATGTATCAATTTGATTCTACTGAA
						GCTAGGTTTGTCTTGTGGCTGCTTCAGTAGACTTGAGATGACTTGATTTACAGTAATCCCTATGT
						GATGTAAGTACTAGTACCTTCCCTTCTCCGCAATCCAGCTCCAGGTTTCAGAAAGTATGCCACAC
						TCAACCTTCTCTCCAGTTCATCCTGTATTAATTTCTCCCATATAATTCAAAGGAGTGGACAGGT
WI-8010	247	GT	---		---	CCCTGGCTGAAAGAAATAAGAGATCCCAAGTGGTGGGG/G/TCTT
						GCCCCGCTATCTTTTAAATTTAACTTGTATCTTTGGTGTTTCTCCATCCTA/GC/GATTCTGCCTTAT
						CTTTGTCTGTCTGTG/GJATTACCTGATTCTACTTTTGATACACAAGGCTGATGGCTCACAATGT
						AGTAGTCCCAATCTTCAGGCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222b	85	GC	---		---	TCTCGACTCTATAACAACCTCCACAGAA
						GCCCCGCTATCTTTTAAATTTAACTTGTATCTTTGGTGTTTCTCCATCCTA/GC/GATTCTGCCTTAT
						AATCTTTGTCTGTGTAGATTACCTGATTCTACTTTTGATACACAAGGCTGATGGCTCACAATGT
						AGTAGTCCCAATCTTCAGGCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222	52	GC	---		---	TCTCGACTCTATAACAACCTCCACAGAA
						TATGCACTTCCACAAAAGCGATATAATTTAAAAGTTTTTTTTCATTAGAAATAAATGTATAAAAAATAA
						ATATGTTATTATAGGCATTTATTACTAATCTATAGTCTCTTGGAAAGGAACACCCCAACCAATACCT
						ATAAAGTACATGTAATTTATAGTAACATATTTTACTATATACATATGGAANAATCATATTCTCACA
WI-8007	242	CA	---		---	GAAGAGCTGAACAGACATTCACCAAGGATACGACTGTTGGAC/GA/GAGCTGCTG
						TCAGTTGCAAAAAATGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGTATGTTTGTAG
						TCATATTACACATATGAGTGAATTTCTG/JGGGCGCATGGAAATACATCTTTATGAGACATTGA
						ACTGCTCACCACATCATAGTATCCATTTAAACAGACCAACAATGTATAGAATCCCTTTGTTTTAC
WI-9823	97	CT	---		---	ATGCTTTCCAATCTGATTTGTATGACTATTGTATGCACAGTTGGATCACC

WI-9651b	105 A T ---	---	TCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCGGAATCCTTTCTCT ACTTGCTCCTCATGTACAAATTTCTGCTGCTCTTCA/ATJGGGGCAGCTTGCAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCTCTG TCITTAACCTGTAAATGGTATATTAATCCTTGGTGTGAAATGCTCTC
WI-9651	139 T C ---	---	TCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCGGAATCCTTTCTCT ACTTGCTCCTCATGTACAAATTTCTGCTGCTCTTCAAGGGGAGCTTGCAAGCCTCCCTTTAGACACCT CTJACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCTCTGT CTTAAACCTGTAAATGGTATATTAATCCTTGGTGTGAAATGCTCTC
WI-7676b	309 A C ---	---	GTGACCTTCTGCAAGCGTGGAGATGGACATCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCTCCAAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCGCTCTCTTGGTGGCTGCTGGTTCAGGGGAGGAGCGTGTGGACTGCAGCTTCTGCTGTGC TCCCGGCTCTGAGGCGAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	GTGACCTTCTGCAAGCGTGGAGATGGACATCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCTCCAAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCG/TTGGCTCTTGGTGGCTGCTGGTTCAGGGGAGGAGCGTGTGGACTGCAGCTTCTGCTGTG GTGCTCCCCGCTCTCTGGAGGCGAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	CATTATCTTGTCTTGGTGTGTTTCAATTCATCTTCTCTCTCCAAATGAAGGATATTTAAGCATCAT CATCTGGCCCTTTTGGAGTTTGAATAATTTTGTG/ATGACTCTATGCACATGATAAATTTGTTA TGCTGTCTCTATCTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAGGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAAATATCTTTT
WI-9986	42 T C ---	---	TTGGTGTGAATCAGAAATATAGGAAAATAAGACAATTTGAAT/A,CJGTACCCAGGAAACAAGAG CCCTGCACCTGACTCCAAAGGAGTTCTATTATTCTGGCTGTTCCAGACTTTATTGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGTAGTACTCACAGAACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAAGCTTATTGCAATT
WI-7041	174 C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGGCACTCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGCCCTGCACATGCAAACTCCAGTCCCTTCCAGAGCTGAAAGGGTCCCTCGGTCTTTTATTT CAGGGCTTGCATGCGCTCTATCCCGCTCTGCTCTCAJCCACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTAAACAAGCTCATTTGTACAGTGTCTTTCATGTAAATA
WI-7224	134 T C ---	---	ATAAACCTTGTGTATGTATCACCACCTCACTAAATATCAACTTATGTGCTATCAGATATCCTCTCT ACCCTCAGCTTATTTGAAGAAAAATCCTAAACATCAAAATACCTTTCATCCATAAAAATGTCAGCATTT /CJATTAAAAACAATAACTTTTAAAGAAACATAAGGACACATTTTCAAAATTAATAAAAAAAG GCATTTAAGGATGGCTGTGATTATCTTGGGAAGCAGAGTATTCATGCTAG

WI-10826	132	A C ---	---	---	TCTATTGCAATTCACAGTAGCCCCATGAAGTAGGTATAACCAGCCTCTATTTTAAATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTCTTAATAAGCAAAGACCTGCAJ/C JCCCTGGCTTCTGACTCCAAAGCTTATCCCTTCTCATGCTGTGTCTGTCAGCCAGGACCCCATGCGCA GAAAGCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145	G A ---	---	---	AGATCTGCCATTAGTATTTATTCCTTTGAAGATACTTTGGAGATTCAATTTCTTGAGTGGCACTGCGAT GCTCATTGAGTGAAGAACTTGTGGGTATAGAAATGGAATGGAGAGTTTCAACAGCTTTGCTGAAAC TGACTTTGG[G/A]CTCCAGACTTCACTGTCTTAGGCATTGAACCATCACCTGGTTTGCACTTCTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24	A T ---	---	---	AAACACAGAAATCATCAAAAGCACJATJATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACCTCTGAATAGTAGGATAGTATATCATTTCTGTATAGATTCACCTCTCAGCAAT TGGTCTGTTTTCATTCTATGGAACCTCTCCGTACTGTAAATTTTCATTCTATGGAAACTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121	G T ---	---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAGAACACATTTTGAATGGTCTTGTC TTTCAATAAAAGAGTGACATGATTGAACATGTGTTTGTAGATAAAGGCACCT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTGAT
WI-4719b	107	T G ---	---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGTGAGCGGATT ATGCTGACGCCATGGGTGTTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTTCATTCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70	G A ---	---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGTGAGCGGATT AT[G/A]TCTGACGCCATGGGTGTTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTTCATTCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216	G C ---	---	---	TCAACAGCCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCCTACCTCTTAOCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGGTGTACCACCTCTCCTGACACTGCCAAAGT TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGCCAGACAGGAGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGAACCGGTTCCAAACTTT
WI-9484	178	G A ---	---	---	TCAACAGCCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCCTACCTCTTAOCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGGTGTACCACCTCTCCTGACACTGCCAAAGT TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGCCAGACAGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGAACCGGTTCCAAACTTT

WI-7330	207	C T	---	---	AGGATGGAAGGAGACACGGGCGAGGAGAACTCTCTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTTTTAAATGTGGCATATAGGTTT GTGACACAAGAAAGTCATACCTTTGGTGGCTAAGTTTACTAAGGAAATAACTGAAAGATTAAAG TGAGAGCTTTGAAAAGAGAAATGATAATGCTTCCAACTGTAGCTGTACAG
WI-9443	211	G A	---	---	TTAAAACAGTTTCAGGTTGGTGAAGCAGAAAAGGATGTGATTACAAATTTAAATGAATCAGTCACCT GCACAAATTAATCCTTTGGCATCATACAACTGGGTTTAAATGGCAATGATGACATCATAGCATGA CCAACTCATGGAAGGCAGTCTAGAGTCCATCAGCTCAGACCTGAGGGGGAAGGCAGTCGCAOCCA CTGACGAGACGAGACGACCTTGGACTACAGATGACACCCACATGCCACTT
WI-7166	59	C T	---	---	TCTCTAAAAGGAGAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA/C/TGGAT CATCAACAAGATTTCCTTTGTGCAAAATATTTGACTATTCTGTATCTTTTCATCTTGACTAAATTCGTG ATTTCAAGCAGCATCTTCTGGTTTAAACTTTGCTGTGAACAAATGTGCAAAAGAGTCTTCCAAT TAATGCTTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCGAG
WI-7259b	189	T C	---	---	GCTTCTCCAGGAAGCGGGTCTTGGCTGGAACTTCCAGAGAGGGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTGGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAAGTGGCCACAGT/C/TJGGGGAGCAG AGCCAGCAGGTGGACAGGTTTTCAGGGGCCCACTTCCCTGGAGCTC
WI-7259	188	G T	---	---	GCTTCTCCAGGAAGCGGGTCTTGGCTGGAACTTCCAGAGAGGGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTGGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAAGTGGCCACAG/C/TJTTGGGGGAGCA GAGCAGCAGGTGGACAGGTTTTCAGGGGCCCACTTCCCTGGAGC
WI-7322	275	A G	---	---	GTACTTTAGGCTGTGGAGGTGGCATTTAGTGTGACCTTGCACCCAGGGTTTCTAACAGATGAC CCTGTGAATCATAAATTTAAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCGTATG GCCATAAACTGCCCTAAGCACTCAGGCCCTCCCACTCATCAACCCCTTTGACCAGAGAAAGCACTC TGGTTCTCTATCCCTTTGTACATAGAGATTGTGATGGGGCTCTGGCTG
WI-7685	46	T C	---	---	TCAGTTCTAGTCTCTGGGGCCACACAGAACTCTTTTGGGCTCT/G/JTTTTCTCCCTCTGGATCA AAGTAGGCAGGAACCATGGACCAGGCTTGGAGCTGAGCCTCAGCTGACTCTTCGGAATACTCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCAGTGGCTTCTCTCTCCCTCTGCCGACTC CTGGGTTGAGCTGTGCTCAGTCCCCCAACAGATGCTTTCTGTCTC
WI-563	87	G A	---	---	TGTGACCAATTGTTATTTAGAGGTTTAAACATGGCTGACTATCACCTGATGGTCGCCAGAATTC CTGGGGGAGGGCTCCCTTGA/JCCCTGATCATGTCTACCTAAGCTGCTACTCTAACAATACTACTCC TGTGGTATGGGGATCCTAAGCCAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCCCTCAGTAAAGGCCAAATTTAAATCTCTTTGGATAACCCAGGGCACAT

WI-931c	191 C A ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCAGTACCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTCTTATTCGTGTGTGTCAAAATGATCCTCT GTTGCTGCACTGTCTACTTGTGTATGGATTTATAATTATTGTCCAAAAAGCC[C/A]CGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTGAGA
WI-931b	81 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCAGTACCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCT[A/G]TCCCTCACCACACCTTCCAGTCTTATTCGTGTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCTACTTGTGTATGGATTTATAATTATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTGAGA
WI-931	31 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCAC[A/G]GCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTCTTATTCGTGTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCTACTTGTGTATGGATTTATAATTATTGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGTGAGA
WI-10870b	91 C T ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCTGTATACAAAATAAGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCCC
WI-10870	103 G A ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGCACTACTTAGA[A/G]CAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCTGTATACAAAATAAGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCCC
WI-7719b	281 T C ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTTGGTCTGGCCAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCCTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTCTGGACATTGCCCATGTATATCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163 A G ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTTGGTCTGGCCAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCCTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATATCTCACTGATGATTTCAAGCTAAA
WI-10396	72 C A ---	---	GCCTTGGAGTATATCTAACTGTGGCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]TGTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTTGTTTTCTTTTGTGA TGCCATTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCCATTGCTGTTCAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94 C G ---	---	---	TCCTTTATGCAACCAAGAGATATTTAATAACACCAATTAACGTAGCAGGGCCATGGCTCATGGGACC CACCCCGGTGGCACTCATGAGGGGGGCGGTGAGGTTGGAACATATGAGTGTCTCCGGCCACACA TCCTGCTGGGGCCCTACCTGCCCCAATTCATCTGCGCAATAAATCTGTCTTATTTGTTTCATCCTG GAGAAATGAAGGGGAGGTCAAGTTGTTGTCAATGATTTGTGACAGAAACCT
WI-7842	57 T C ---	---	---	CACAGCCATGCCCTTGAGGAGCCGGCCACACAGATGCTGTAATCCCTATCCCATCTGTCGTATGAG TCCCATTTGGCTTGCAATTAGCAATCTGTCTCCCCCAAAAGAAATGTGCTATGAAGCTTTCTTCT ACACACTGTGAGTCTCTGAATGAAGCTGAAGCTCTTAGTACAGAGCTAGTTTTCAGTGTCTCAGAAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---	---	---	CTGCTCATCAGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCAAGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCCCACCCAGCTGTACCCAGCCGGGAGGTGCAGCCCTTCTCTCC TGCTCTGC[AC]TCTGACTCTCTTTTGAGGTCCTGTATGTCTACCTGACTTCTGTGGTCCCTCTG TGCTGCTCTCATCATCTCTTACTGGGGCTGGGGCTCTAGCCCAA
WI-4767b	173 C A ---	---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCT CAGGTCTGGTAATCCTAGATCTTCTATATCAATGAGTGTGAGTGTGAGAGAGGGTATGTTT CTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACA[CA]AATCACTAAGGAATTCACACTAAGA CTCCTCTAACCCAGAGATTTTAACTT
WI-4767	50 A G ---	---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAA[GA]ATTCATAAAGAGTT CCTCAGGTCTGGTAATCCTAGATCTTCTATATCAATGAGTGTGAGTGTGAGAGAGGGTATG TTTCTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCACACTAAGAC TCCTCTAACCCAGAGATTTTAACTT
WI-7718f	222 C T ---	---	---	ATTGCACTGAAGTTTTTGAATACTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTGAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[CT]TCATGCAGGAAGGAAACTATGTATTAAT
WI-7718e	60 T C ---	---	---	ATTGCACTGAAGTTTTTGAATACTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGA[TC]GCAA GGATTACAGAAACTGATGCCAAGGGCTGAGTGAAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTGAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAT
WI-7718d	31 G A ---	---	---	ATTGCACTGAAGTTTTTGAATACTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAAACTGATGCCAAGGGCTGAGTGAAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTGAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAT

WI-7718c	91 C G ---			ATTGCACTGAAGTTTGTAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCGTGTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718b	248 A G ---			ATTGCACTGAAGTTTGTAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718a	42 A T ---	C		ATTGCACTGAAGTTTGTAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGTC AAGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7227d	99 G C ---			AGGGAATTGTGTGCTCCTGGAGGAAGCCAGGCCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCGAGAGGGACTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---			AGGGAATTGTGTGCTCCTGGAGGAAGCCAGGCCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC GGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCGAGAGGGACTGAGCTAAACAGTG TTATTATGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---			AGGGAATTGTGTGCTCCTGGAGGAAGCCAGGCCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCGAGAGGGACTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---			AGGGAATTGTGTGCTCCTGGAGGAAGCCAGGCCATCATTAACAAGCCAGTAGGTACCTGGCTTC TTCCGTGGACCAATTTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCGAGAGGGACTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---			CCACAATGCCCTCCACAGTGTCAAGGACTCCTGTCTGCTGGAGGTGGGAGACAAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATCGAACAACCTGATGCGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACCTGAGCCAAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCATCCCAACATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCTCTGTCTGTCTGAGGTGGAGACAAAGGAACCTT/A JCCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCTTCATCGAACAACTGATGCGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGACATGTCTATTGAACTGAGCCAAACACACTGT AAATATCCACAGACTCTCCCTGCCCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	CCAGCAACACCTACACCTTTGTACCTGCTGGACTCTATGATGGCTGTGGTTGATAATAATCA GATCATGCCCAAGACGGGCTCTCTGATAATCGTCTTGGGCATGATTGCAATGGAGGCAATGCGTCC CTGAGGAGAAATCTGGGAGGAGCTG/GAGTGTGATGAAGGTGTATGTTGGGAGGAGCACAGTGT CTGTGGGAGCCCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7878a	51 C G ---	---	CCAGCAACACCTACACCTTTGTACCTGCTGGACTCTATGATGGCTG/GGTGGTTGATAATAA TCAGATCATGCCCAAGACGGGCTCTCTGATAATCGTCTTGGGCATGATTGCAATGGAGGCAATGC GTCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGGAGGAGCACAGTG TCTGTGGGAGCCCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAACTA
WI-7381c	213 C T ---	---	CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTCTCTTCTACC AGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGACAGTTTCTGCTATGTTGAGATC AGATGTGCCAAGGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAACGGCTCTCTGGCTCTCAGAGCATAATCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTCTCTTCTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGACAGTTTCTGCTATGTTGAG ATCAGATGTGCCAAGGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTCTCTTCTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGACAGTTTCTGCTATGTTGAG ATCAGATGTGCCAAGGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	AAATTGCTCTATTCCGACCCTCATATTAAATAGAGCAATGAGAGCGAGGAAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAAAG/GAGATGTAGATTGTACATTCAATCTGAAACAAACCTG CCAGGCAAGTCTCTTCCCATTTACAAATAAGGAGACAAATTTAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGTGAGTTTGTGCC
WI-1017a	92 G A ---	---	AAATTGCTCTATTCCGACCCTCATATTAAATAGAGCAATGAGAGCGAGGAAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAAAG/GAGATGTAGATTGTACATTCAATCTGAAACAAACCTG CCAGGCAAGTCTCTTCCCATTTACAAATAAGGAGACAAATTTAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGTGAGTTTGTGCC

WI-1795b	130	T C	---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTTCTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGTCTTGAGAGAAAGAAAGT/CJC GTCTACCAATTTTCAACAAATTCGTAGTACAATTTAAGTATCTCTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47	T C	---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTT/CJCTTCCAGACTCCTACGGA TTAAATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGTCTTGAGAGAAAGAAAGT/C GTCTACCAATTTTCAACAAATTCGTAGTACAATTTAAGTATCTCTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136	G A	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCGAGCATCATCAGCCCGTTAAGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGTCTCTCCATACGTAGTCTGTTCTCTCTATCAGATTGCCA C/GA/TAGCCCTCCCTTCCCTTCCCTTCCCTTCCCTTCCAGGCCCTTTCAGGCCCCAGTCCCTCTGAGACTCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616c	136	G A	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCGAGCATCATCAGCCCGTTAAGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGTCTCTCCATACGTAGTCTGTTCTCTCTATCAGATTGCCA C/GA/TAGCCCTCCCTTCCCTTCCCTTCCCTTCCAGGCCCTTTCAGGCCCCAGTCCCTCTGAGACTCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616b	141	C T	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCGAGCATCATCAGCCCGTTAAGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGTCTCTCCATACGTAGTCTGTTCTCTCTATCAGATTGCCA CGTAGC/CJCTCCCTTCCCTTCCCTTCCCTTCCAGGCCCTTTCAGGCCCCAGTCCCTCTGAGACTCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616a	116	G C	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCGAGCATCATCAGCCCGTTAAGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGTCTCTCCATACGTAGTCTG/CJCTCTCTATCAGATTG CCAGTAGCCCTCCCTTCCCTTCCCTTCCCTTCCAGGCCCTTTCAGGCCCCAGTCCCTCTGAGACTCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-1126c	52	G A	---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTCCAGTATCACTG/AJATACTAATAA AAACCCTGTAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATTTAATTTCAAGTTTCTCAAAAGGAATATGAAAT TGTTAAATGCAATCCAGCTGTAACTTTTTGGACTTGCTTTTATTTCTT
WI-1126b	230	T C	---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTCCAGTATCACTGATATAATAAAAA CCCTGTAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAAAT TTATTTCTCAAGATATAAAAAATAAATTTAATTTCAAGTTTCTCAAAAGGAATATGAAATTTGTT AAAATGCAAAATCCAGCTGTAACTTTTT/CJGGACTTGCTTTTATTTCTT

WI-1126a	97 T C ---	---	CTCTATTCTCTGGGCACTGCTTCTTTGGGGCAAACTTCCAGTATCACTGATACTAATAAAAA CCCTGTAAGTCTGCTGCAATTTCAAGATTC/CAATATATATCCAGATTGTTTTCCAGCAAGAAAA ATTTTATTTCTCAAGATATAAAAAATAATATTTAATTCAGTTTCCCAAAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACITTTTTGGACTTGCTTTTATTTCTT
WI-11183c	124 C T ---	---	TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTTAAAAATCTTTTTAACTTGAAAAATTTAGAGTAC ATATAAATAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTTTGCCCTTGTCACATAACATTT TTTATGACATAGAAATGACCAAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---	---	TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTTAAAAATCTTTTTAACTTGAAAAATTTAGAGTAC ATATAAATAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTTTGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---	---	TAGTGCTAAATTTTGGAAAAGTTTGCTGATTTTTAAAAATCTTTTTAACTTGAAAAATTTAGAGTAC ATATAAATAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTTTGCCCTTGTCACATAAC TTTATGACATACAAATGACCAAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---	---	GCTTGGTTTGCTTTAGTCTTATTGCTCAGTCTGAGTTCTCCCTTCTGCGCTGGCCCTTTTGTATTCA CCCATACCTCTATGCTGCTGCTCAGACCAATTCCTCTATCTGAGCGCTCTTCTGTACTTCTCCTG TTCACCAACCTTCTTTTATCTTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTCTTCC
WI-10770a	49 G T ---	---	GCTTGGTTTGCTTTAGTCTTATTGCTCAGTCTGAGTTCTCCCTTCTG/TCCTGGCCCTTTTGTATT TCACCCATACCTCTATGCTGCTCAGACCAATTCCTCTATCTGAGCGCTCTTCTGTACTTCTC CTGTTCAACCAACCTTCTTTTATCTTTCAGGACACTCAGTTACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTCTTCC
WI-9667b	82 C T ---	---	GATGACAACTTCTGCTGACCCCTTAGTCTTGTCTCAGTCTTCAATCTCTGCTTGTATCATGG TTATCACTGGACA[C/T]AGCCACCTCCAGAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGTTATTACACACAGTATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT
WI-9667a	68 G C ---	---	GATGACAACTTCTGCTGACCCCTTAGTCTTGTCTCAGTCTTCAATCTCTGCTTGTATCATG G/C]TTATCACTGGACACAGCCACCTCCAGAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGTTATTACACACAGTATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT

WI-10400d	189	A G ---	---	ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATATTTTATTCTAATTTT TCCTTCCCTTACCTTTAGTCTCTCCACCCAAAATAACGTAAGTACCTATGTCTAGTGCCCATGTAG TTTTTGGTTCAATTTAGTCTGCAAAATTTTCAAAAGCGTTAATGCAATTATG
WI-10400c	166	A C ---	---	ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATATTTTATTCTAATTTT TCCTTCCCTTACCTTTAGTCTCTCCACCCAAAATAACGTAAGTACCTATGTCTATGCCCATGTAG TTTTTGGTTCAATTTAGTCTGCAAAATTTTCAAAAGCGTTAATGCAATTATG
WI-10400b	165	A G ---	---	ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATATTTTATTCTAATTTT TCCTTCCCTTACCTTTAGTCTCTCCACCCAAAATAACGTAAGTACCTATGTCTATGCCCATGTAG TTTTTGGTTCAATTTAGTCTGCAAAATTTTCAAAAGCGTTAATGCAATTATG
WI-10400a	46	T C ---	---	ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATATTTTATTCTA ATTTTCTTCCCTTACCTTTAGTCTCTCCACCCAAAATAACGTAAGTACCTATGTCTATGCCCATGT AGTTTTTGGTTCAATTTAGTCTGCAAAATTTTCAAAAGCGTTAATGCAATTATG
WI-10809b	78	C T ---	---	AAAGGCTACAACTAAGGCCAAACCATTGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTACCA/C/T/TAGAAAGGGCATTCAAGCACATTCATGAGGCTTCATATACCTGTTAG CAACAAATGGAATGTATTAGCCAAAGCGAGGTATGGACCAAAAGTCCCAAGTATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGTATACACATGACATAGGCTTAA
WI-10809a	33	C T ---	---	AAAGGCTACAACTAAGGCCAAACCATTGAACGGTATAAGGAGGGTAAATGCAAGGGGAGAG CCCCAAGTCTACCACTTAGAAAGGGCATTCAAGCACATTCATGAGGCTTCATATACCTGTTAGC AAACAAATGGAATGTATTAGCCAAAGCGAGGTATGGACCAAAAGTCCCAAGTATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGTATACACATGACATAGGCTTAA
WI-7038c	266	T C ---	---	CGAGCTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTTCCTGGCCACATCCAGCTTGTGTCC CAATGAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAC AAGAAGACTGTAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTTGAT CATTTTATATGAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140	A C ---	---	CGAGCTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTTCCTGGCCACATCCAGCTTGTGTCC CAATGAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAC AAGA/C/GACTGTAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTT GATCAATTTTATATGAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGTA

WI-7038a	31	G A	---	---	CGAGCTTGGGATAAGCAAGGGGACCTTGGGGA/CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAATAGTACTGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACACGACATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCCTGCATTATGGGTAGTTCTGA
WI-3429b	64	G T	---	---	ATACGCTTCTGTCTGCCACAGTGAACAGACACCCAGGTGGCCAGGGTGGGCTCCACACA(G/T) CCCTCAGCCCCCTCAGCTTTCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATCCAGTCTCCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	---	ATACGCTTCTGTCTGCCACAGTGAACAGACACCCAGGTGGCCAGGGTGGGCTCCACACA(C/T)AG CCCTCAGCCCCCTCAGCTTTCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATCCAGTCTCCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAAGTGACGGTGACCT GTGAGCCCCATTCTTGTG/AJTGGAATAAGGTGTCCATTGTTCCTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCTCTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6786b	111	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAAGTGACGGTGA CCTGTAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCCTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCTCTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6786a	106	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAAGTGACGGTGA CCTGTAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCCTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCTCTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6711b	226	G T	---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCCAATCACTCTGAAT TTCATATACCTCCATTATTAATTCATATACATCATTCAGAGAAAGACAACGGTGCCAACTGGGTT TGGTTGGTGGCTGCACACCCACA(G/J)TGGCAACTAAGTGAATCTCTAAA
WI-6711a	361	T C	---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCCAATCACTCT GAATTCATATACCTCCATTATTAATTCATATACATCATTCAGAGAAAGACAACGGTGCCAACTG GGTTGGTTGGTGGCTGCACACCCACAGTGGCACTAAGTGAATCTCTAAA

WI-10613b	172 A C ---	---	---	ATTGATGCCAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTATAGAAATTTTGAGCCATA TGGTGAAAATTTAGAAGTATTCTCTATATGATATATCTAGTTTAACATCAATGAATGTGATTT TTTGCAACTTTTGACAGGCCAGGCAATTTTATTGACJGCCCCTAGGAGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44 G A ---	---	---	ATTGTATGCCAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTATAGAAATTTTGAGCC ATATGGTGAAAATTTAGAAGTATTCTCTATATGATATATCTAGTTTAACATCAATGAATGTG ATTTTGTCAACTTTTGACAGGCCAGGCAATTTTATTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133 A T ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAGATCTGTGCTTTCCAAAGTGACTACCCCTTGAAGC ACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAAJA TJGGAATGAACCACTCCCTGCCATTCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587b	81 G A ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAGATCTGTGCTTTCCAAAGTGACTACCCCTTGAAGC ACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCTCT TCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587a	28 C T ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAGATCTGTGCTTTCCAAAGTGACTACCCCTTGA AGCACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCTCT TCCACATGCCCCCATATGTCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-10681b	103 T A ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAAAC ACAGAAAAGCTAAAGACATCCTTTTAAAAAAGCCTTAAAGACAGCCATTTTAACTCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGAGAGGAGTGACGCTCTGTAAAG
WI-10681a	41 A T ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAA ACACAGAAAAGCTAAAGACATCCTTTTAAAAAAGCCTTAAAGACAGCCATTTTAACTCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGAGAGGAGTGACGCTCTGTAAAG
WI-7222c	126 G T ---	---	---	GCTCTCTCAACTGCTCTGGACCCAGGCTAGGAGGCTGCTTGAATGACTGTGGTCCCTCT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCTGTTCTCAAGTTGGGGATGGG(GT)AATAA AGGAGGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGATTTTCAAGACTCGAATTCATTTT

WI-7222b	255	G A	---			GGCTCTCCTCAACTGTCTGCGACCCAGGCTAGGAAAGGCTGCTTGAGATGACTGTGTGTCCTCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGGGAATAAAGG AGGGGAATTCCTTTGAACAAGAACTGGGGATAGTTATATTCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGAAGGTTGATTTCAAAGACTCGAATTCATTTCTCA
WI-7222a	126	G T	---			GGCTCTCCTCAACTGTCTGCGACCCAGGCTAGGAAAGGCTGCTTGAGATGACTGTGTGTCCTCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG(G/TAATAA AGAGGGGGAATTCCTTTGAACAAGAACTGGGGATAGTTATATTCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGGTTGATTTCAAAGACTCGAATTCATTT
WI-8054d	41	C A	---			AAAGATGACACTTGAACCTGGATCACTTGGCCCTTCTCTCTTCA/JTTATCTCTCCAGTTCAAATG CTTGATCTTTAATAGCCAGCATTTCTTAGATCTGAGTTGGCTCAACGCACCTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGGCCACCATTAGCCACTCTGCT TCTGTCTATAACGCCGCTTCCCTGGCGGTACAGAGAAATCCTTGGCCCTT
WI-8054c	237	G T	---			AAAGATGACACTTGAACCTGGATCACTTGGCCCTTCTCTCTTATCTCTCCAGTTCAAATGCTT GCATCTTTAATAGCCAGCATTTCTTAGATCTGAGTTGGCTCAACGCACCTCAAGCCTTAGCACAA TCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGGCCACCATTAGCCACTCTGCTTCC TGTCATAACGCCGCTTCCCTGGCGGTACAGAGAAATCCTTGGCCCTT
WI-8054b	148	T C	---			AAAGATGACACTTGAACCTGGATCACTTGGCCCTTCTCTCTTATCTCTCCAGTTCAAATGCTT GCATCTTTAATAGCCAGCATTTCTTAGATCTGAGTTGGCTCAACGCACCTCAAGCCTTAGCACAA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGGCCACCATTAGCCACTCTGCT TCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGGCCACCATTAGCCACTCTGCT TCTGTCTATAACGCCGCTTCCCTGGCGGTACAGAGAAATCCTTGGCCCTT
WI-8054a	131	C G	---			AAAGATGACACTTGAACCTGGATCACTTGGCCCTTCTCTCTTATCTCTCCAGTTCAAATGCTT GCATCTTTAATAGCCAGCATTTCTTAGATCTGAGTTGGCTCAACGCACCTCAAGCCTTAG(C/G)A CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGGCCACCATTAGCCACTCTGCT TCTGTCTATAACGCCGCTTCCCTGGCGGTACAGAGAAATCCTTGGCCCTT
WI-10854b	152	G T	---			TTCCACAAAACTTCCCTGGCCGGGTGACTAAGATGAGAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTACTTTAAGCGAAGTTGAAACACGAAAGATAGTTAACGCTGGTAAGTTTAT ACGGTGTGCGAGGCAACA(G/T)GGAGAGGTACGGGAATAGTTCTACTTCTGTTTATTTCTTG TTTTAGACACAGGGTCTGCTGTGTTG
WI-10854a	102	C T	---			TTCCACAAAACTTCCCTGGCCGGGTGACTAAGATGAGAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTACTTTAAGCGAAGTTGAAACAC(C/T)GAAGACGATAGTTAACGCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGAGAGGTACGGGAATAGTTCTACTTCTGTTTATTTCTTG TTTTAGACACAGGGTCTGCTGTGTTG

WI-9826b	127 GA ---			<p> AATTTTATATGTAAGGGTTAGCAAACTATGGCCACAGGCCATTCTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTGGTGTTCACGCGAGTTGAGCCATTGTGACAGAGGCTGTATG/AIGCCTT CAAAGCCAAAATAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATCTAGATATTTAAA GGCAGAGAAGATCAGAAGTGTGAA AATTTTATATGTAAGGGTTAGCAAACTATGGCCACAGGCCATTCTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTGGTGTTCACGCGAGTTGAGCCATTGTGACAGAGGCTGTATG/AJGGCCTTC AAAGCCAAAATAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATCTAGATATTTAAAAG GCAGAGAAGATCAGAAGTGTGAA </p>
WI-9826	125 A T ---			<p> TGACATTATAT AAACGTAAAA GAAATGT </p>
WI-15986	60 T G GTGGGTTTT	TTTGTGTTGT		<p> CGGACACGTGTATATACAAATACAGATCGTATGGGTTTGTGTGTGGGTTTTTTTTT/GJTAC ATTTCTTTACGTTTATATAATGTCAGCATTTCAA </p>
WI-8655	29 A G AG	AAC TGCAAAAT AGGAAACCAG		<p> TTCAAGTAACTGCAATAGGAAACAGAG/AJGGGAGGCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGAGGAGGTGGCCCTACACCCCTTAT </p>
WI-8170b	259 GA ---			<p> GCACTTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACGAAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA </p>
WI-8170a	204 T A ---			<p> GCACTTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACGAAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAGTGCAATCCTATCAATCAGAA AT/AJAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAC </p>
WI-8172	136 C G GACA	CCTTTATTA ATTGTTTTCTT		<p> CAGGATTCCTTAAGTCATCTTCCAATACTCCAGGTACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCAATTAACAAGCTTTTAAATCTCTCGGTAACTCCCTTTTATAAAATGTTTCTTGACAT A/C/GJAGTACCTTTACAGGTATTACATTCTCTCACCGTTTACA </p>
WI-8183	56 GA TGC	TGAAATAAAA ACAAATTTCTGT		<p> AGCAGGGTTTGAATGATCCCTTATTTACATGAAATAAAACAATTTCTGTTCG/AJGCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGCTCGTTCTTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC </p>
WI-14149	83 CT ---			<p> GCTTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAACCCAGCATGGGATTTTGCCGGAAT ATTAGCGTTAAAGGAG/C/TTGAGTTGAGTCAACACGCGG </p>
WI-8712	44 G A G	CACAGGGAAG AGGTAGTGA		<p> TCAACAATGACACTGTGTACAGCACAGGGAAGAGGTAGTGGAG/AJGAGATGGTCAGGCTTCCTG TTCCTTAACAGCAGAGCCCCAGCAACCTAGAAAGCCCTCACCTAGCCTCTTAAT </p>

WI-8827	22 C T	TCCCTGGGAG T TTAGTGTTCA C	GCGATTAGGAT T TTAGTGTTCA C	GGTGCCCTGGGAGACTATGGC/TAGTGAACACTAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTTCTTAGTTCCTTCTTATCCACCCAGTCTTCT
WI-8833	51 A T	TCTTCCATGCC A T T TCTCTG	CCTCACACATT ATAGGGCA	CTCCGGCTCTTAAAGCTCTGTAGACTGTCTCTTCCATGCCATCTCTG/AJTJGCCCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACCTGCCTTGTCTATAAAAGGTGAGCTATGT
WI-8377	63 A G	GGGACTTAAC C T T TGGCCT	CAACAGCCA GGCAGG	ATTTTTAGCCATGTTGGTAAAGTTCAATTTTCAGTACATGGGTAAACCCAGGCCCTTCCC/AGJT TATATCCAGGTATGCTACAAGTTCTTTAACTCTTATCAGAAGTTATTACTGTTCCTTAGAGAG GCTACCAGGCTAAATTCACCTTAGTTGGTTGTCTAATGTCCTCATTATTTATCCTGAAGCTCGTG
WI-8850	21 A G	CCGGGCATTG C T T AGGATA	AGTCTTCTCTGA GGCTTCCAT	GAGGGACTTAACCTTTGGCCT/AGJCTGCCCCGTGTTGGCTCTGGCTGTCTGCTGCTGCT TCTCTTCTAGTGGTCTTTCTTTGTCTTTGCCAGCCACTATGCTGCTGT
WI-8853	79 C T	CCGGGCATTG C T T AGGATA	AGTCTTCTCTGA GGCTTCCAT	ACTTTCTTGAGCTGAGCAACCTCATCTCTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA/C/TATGGAAGGCTCAGGAAGACTTCTCTCAA
WI-8865b	52 A G	CACAGACTGA GGAAGACAGT	GGTAAGTCCGA AGCATGTTG	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA/T/CJGGTGAACAACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTCCATATAA
WI-8865a	42 T C	CACAGACTGA GGAAGACAGT	GGTAAGTCCGA AGCATGTTG	GTCCACAAACCTGGACACCAACCAACAGAAT/CJCTCCCGCTCTTTGAAATTTCCATTAAAGAGCA CAATGGGGTAATTATACCAAGGATGCTCCATCGCTCTTC
WI-8895	32 A C	CACAGACTGA GGAAGACAGT	GGTAAGTCCGA AGCATGTTG	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATTTGTGAAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCAAC/AGJTTATGTCAAGTTAATAAACAATTTCTAAGTGTCTCAGTC TCAACTTCTGTGTTATCTTCCATGGTCCAGTAACAGTTCAACGGCAGACCAAGTTGTGTAGCAG TGGCATAGACGAGGGCTTCTCAAACCTCCGCTGCTGCTCAGTCAACCCAC
WI-8456	93 G C	CACAGACTGA GGAAGACAGT	GGTAAGTCCGA AGCATGTTG	TTTCATCATCAAAAGTTTCTTCCATAGAAGAAJGGTAATGTTGTATCAGTGCATATTTCTATGAAA ATTATATCTCAAGTAAGTAACTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGTCA AAGACACAATGCTGCCAATGCA/AGJTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496b	157 A G	CACAGACTGA GGAAGACAGT	GGTAAGTCCGA AGCATGTTG	TTTCATCATCAAAAGTTTCTTCCATAGAAGAAJGGTAATGTTGTATCAGTGCATATTTCTATG AAAAATTCATATCTCAAGTAAGTAACTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAGACACAATGCTGCCAATGCAATGATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT TGTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A	CACAGACTGA GGAAGACAGT	GGTAAGTCCGA AGCATGTTG	CTGCAGGTCTATGTGCAGGAAGGCCAG/AGJTCCTCTGCGGTTGTCAACCCACATCCACAGAGCA GGCTAGTGCCAGGTGCAGCCACTGCCACCCACGGCACACGGGAACAGGCCCATGCTGC
WI-14153	28 A G	GTGAGGAAG GCCAGC	AACGGCAGGA GGGGA	

WI-12108	40 C T A T A	TGGAAGGG TTAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAAGGGTTAAACTCAAATATC/TJGAAAATACTTTTCATTATACCAGGT CAAGAAAATGCCACAGCCAGAAAAATTTATTTAA
WI-5989	29 G A CACAGGCA	CCCAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAACGTCACAAAGGTCACAGGCA/GJCGTACATACGGTCTGTTATACCCCATATATTAC CCCTTCATGTCTAAAGAAGACATTTCTCTTAGAGATTTTCAATTTTAGTGATCTTTAAAAAAAAT CTGTGTAACTTGCTCCATCTTTTCTGGGTGAGGACAC
WI-12201	61 C T C T G C A T G	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGCC	ATAGTCTTTAGCCTTTTCTCGGAGTGTATGTCOCAGGCCACTGATCACCTGCGATG/CJTGCCA GGTATGGTGGGGTGTGATGGACGTGGTTTCAGCCCTCCTCGATAAAAGGC
WI-12018	31 A T TCTGACTT	GGCAGCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAAGCAGCCTGTGACTT/AJCTCTCTGTTCTGTCTCTCTCTCCCCACATACCA ACTTCTCACCATGATGATTATACCAATAATACAGTTCTTATATGAGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGACG
WI-14162	57 A G C T C	TGGCTCGCTG	AGGGATCAA GAGAAAAGGC	TTTTCTGTTTAAATGATCCGAATGCTTGAGAAGAAACCCCTGGCTCGCTCJAGJGCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92 A G T T	CATGCCCTTTA AGGATTAAGT	TCCTTTCTCTTT TGGTAGTGGG	AGCATGTAAGGAGCAGTTTTATTGATTGGTATATTAGTTCTTAACCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAAGTTAA/GJCCACACTACCAAAAGAGAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109 T C A A T T	GTTGAGTATT GTTCTGCTCAT	GGGAAGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTATTCTGATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTGTTCTGCTCATAAATTT/CJCCAATATGTACCAGACCTTCCC
WI-12326	25 G A C A	GACAGACTTC AAAAGCAATT	AGGTTTGAAAA TATGTATTAAAG TACTTTGT	CTGACAGACTTCAAAGCAATTAC[GJ/CJCTCCAGAATACAAAGTACTTAATACATAATTTCAAAC CTGTTTGCATTTCAAACAAGTTAGCGTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63 C T ...		---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATAGGAATTTTCAGCATATGTATTATC/JT TGAACATAATTTACAAAAGTGGACAGTTGGAAGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87 C T A T C A C A C C A	CAGACACAGC ATCACACCA	GAOCCCTCOGT GGGC	ATACTGGTTAATCCATGTCACACCA/CJTAGGGCCCCACGGGAGGTGGGAGACGACACTTTTCCCTGGG ACAGACAGCATCACACCA/CJTAGGGCCCCACGGGAGGTGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67 A G T T T T	GGGAGGAAAA TCCAATAAAT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTTCTGGTGAATCTTTTAAAGCAGGAGGAAAAATCCAATAAATTTTTTAAJ AVGJAAGGTTTAGCTATTCCCCAATGCTATTTAATAACAATTGAGGTTAGGACGTTAAGTCTTATCAGA CTGTGTAAGTTACAAAAATGATCTGAAGAAGTTATCTGTTCTTGTC
WI-11324	40 C G T G T G C C C A	GGATAAATCA TGTCGCCCA	ATCAAGCTTTG GGCTCT	AGCATACTGCATCTCTTTATGGATAAATCATGTGCCCCA/CJGAGAGCCCCAAAGCTTGATGACAT TCTGTAAGTTACAAAAATGATCTGAAGAAGTTATCTGTTCTTGTC

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WI-14186a	52	C T A	GGTCATTGAT GGAAAGACAC	AACATAACCA CCTGTAATTT GTACC	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCATTGATGGAAGACACATAC[CT]GGTACAAAATT ACAGGTGGTTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTTGGCTATAGGTGCTTCTAAACTTGAGCTTGCAGAGAACACTTGTGGGCTT[A] GTTCAAACATGGACTGATAGTCCACCCAGATTTCTAACTGGGTAGGCTGGGGTG
WI-12345	37	C A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCTGACCAGCTGGGCTTGGCAGCTTTGTGAGATTTGCAAAA
WI-13416	71	C A	AAATTTTGG AAGTTTTTCAG	AGTGTATTAG TTCAATGAATA ATTTCAA	GAAAGGCTGTAATTTTATTTCAAATTTTGGAAAGTTTTTTCAGAAAAAAATAAAATGACAAGAACAA CATA[C/A]AAATATTGAAATTTATTCATTGAACATATAACACTTAGCAGAGGAAGGACTTTTGTAT
WI-12310	46	G A	TTATCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTTGGTCTT AAA	TTTGAAAAGATGCTGAATTTATCCCAAGTATAATTTTAAAAAGCTT[G/A]TTTAGGCCCAACACATA TTTAAACATCTCTTACACATACAGAATTTTCAGTTTACAAATATTCCAGAAAGGCAATTTTCTTAAGCAG T
WI-12086	72	C T	CCGGGAAAC TTGGATT	GGAGTCTCGG GTCTGG	GAAACGAGCTTTATTGGAGCAAGAGTGGGACACTGTTTACACAAAACGTTTCCGGGAAAACCTTG GATTTCTCCAGACCCGGAAGACTCTCCCAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCGCTTAGCT
WI-11549	102	T G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCOC	ATGTCTTCACAGGTGTATTTTGTAAAGAGTTTGTCTATCTAAATTTTCATATTTATTGGCATAAAGT TCATAATATTCTTTTATGATCTTTTAAATATCTGT[G/GGGGATTTGTACAGACTTTCCIC
WI-11585	79	T C	TGGGTTTGCA AAACAAA	CCATGCTTCAC TGATCTTCC	TTAGAGGAAAGAAATAAAACACACGTAATGGGAAAATCAGTTTCAAGGTAGGAGGAAAGCTGGGT TGCAAAAACAAAAT[C/GGGAAGTATCAGTGAAGCATGGCCTAGAAGTCCAAGAGCAGGGGTAGAGT TT
WI-11604	68	G C	---	---	TTAGTTGGTTTCTGAAACCTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT G/CJAGAACTAGGGACTTTTCCATGAAAATAATTAAGAGCTAAGGAATTTCTGACGCTCACCATTTC TTTGTACTCTGCAGTT
WI-11614c	108	C A	---	---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAGTAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCA[C/A]ATATTAAGTATTCGTGAGCTAC GGACTTGGT
WI-11614a	60	A G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGOC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAGTAAATCCAGAAAGACTCAGCTGCTTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTGAGCTAC GGACTTGGT
WI-11626b	83	T C	---	---	TTGATTTTACTAAGGTCTCCACTGGAACATGAAGGTAGGGATAAGGTACAGGATAATATATCTCAG ATATTTTAAAATAAAAT[C/JTACTTAAATAAGAAAATTAGCCATACCACATTTGTTCCATTTGCTAG AAGAACAAAATTGGCAATGA

WI-11626a	39	G A G	T C A C T G G A A C A T G A A G G T A	G T G G T A T G G C T A A T T C T T A T T A T T A A G T	T T G A T T T A C T A A G G T C T T C A C T G G A C A T G A A G G T A G [G] A G A T A A G T G T A C A G G A T A A T A T A C T C A G A T A T T T A A A A T A A A T T A C T T A A T A A G A A A T T A G C C A T A C C A C A T T G T T C C A T T T G C T A C A A G A A C A A A T T G G C A A T G A
WI-11627	23	T C A	C C T T C C T T C C C A T T G C A A C C C A T C T C A A G	C A T T T G C A A C C C A T C T C A A G	A C C C T T T C C T T C C A T T G T C C T C T [C] C T T G A G A T G G G T T G C A A T G G G A A G T A A A G C A A A A A G G G A G A T G A G A A A T A C T G A T G C C T T T T G T G T G C T T A C T T C C A T T C G C A T G T C A A G T C C A T C C A T G
WI-11636	61	A G T C C T	G G A C T T A A A A A G A T C T G C T T A T C C T	A G A A C T T G C T A A A T A T T T T A T G T A A C A C T	T C A G A A A T G T T G C A A G C A A A T A C T A T T T G T A A A G G T G G A C T T A A A A G A T C T G C T T A T C C T [A] G J T A T A T C C A C A T A A C T C T A G T G T T A C A T A A A A T A T T A G C A A G T T T C T G T G A C A G G T C T C A G T A A A C A C T T T G A C T C C T T T T T G G T A
WI-11537	119	C G T	A T T G C T C A T C T T A C T C T G A C C A	G A C C C A G C A A A A G A A T G A T T	G T A C C A T T C T T A T G T G G C A A A T A A G C A A A C T G T G A G T A A C G A G G G C A G C T G A A T A A A T T A C A G T A T A C A A T A T T A G A G A A T A T T A T G T T G C A A T T G C T C A T C T T A C T C T G A C C A T [C] G J A T A A T C A T T C T T T T T G C T G G T C C A G G A O C
WI-11654	37	G C C T G	G C C A A A A G A C T A T T C A G C A A	G G C T C T C C A G G A C A G T T T	A G T A G A A C A T C A G T G C C A A A A G A C T A T T C A G C A A C T G [G] C J A A A C T G T C C T G G G A G A G C C A C T C C A G A G C T A T T C T A A G A C T T T C T G T G T G T T C A T A C T C T A C T A C A G A G T T C A C A C T C A T A T T T C A T A T T T T T A T T T T G G G T G T G G G T
WI-11656	28	G A A A	A T T G A T T T T A G A A G G A A C T G C	C A A G G C T T T G T C C T C A A G T A A A	A C C T G A T T G A T T T A G A A G G A A C T G C A A [G] A C T T A C T T G A G G A C A A A G C C T T G C C T G C A G T T G T T T A A A T G T C C T G A A C A A T C A G A T T C C C A G C C T G G A T
WI-11680	55	T C --		---	A C A G A T A C T T T C C A C G C A A C A T T C T G A A T G A A G C T T G A T T C T C C C C T T T T [C] J T T G C A T A A A G G C T G G G A A G G T G T T T G G C C A G A C C G T A C A T C T T T T
WI-11696	47	T C A G G G A C A G	T T A T C A C A G C A G G G G A C A G	G G C A T T A G A G A A G C C A A C C T T	G T C C A A G A A C A A A G A T A C T T T G A C A T C T T A T C A C A G C A G G G G A C A G [C] A A G G T T G G C T T C T C T A A T G C C C A C C A T C T T G T G T T T C A G A A T C T T T C C A C T T C G C C
WI-11702	69	C T C A G C A G	G A A T A A T A C T G A A A T A A C C A	A G A A C A A C T T A A G C A A A T T A T	T T A C A T G T G G T C A A T G G T G A C A T A C T T T C A A T A A T A A A A T C G A A T A A T A C T G A A A T A A C C A C A G C A G [C] T T T T C A G T A T A A T T T G C T T A A G T T G T T C T A G A A A C A C T G C T A A T T T T T G T T T C T G C A G A
WI-11706	60	C T T C T C T C T T	T G G C T G G A A T T T T C T C T C T T	A T C A C C A A A G A A C A A A T T C C A	T G C T G A T T C A T C G C T T C A C C A T C T G G C T G G A A T T T T C T C T T C T T G T A C A A T T A T T T G C [C] T G G C T G G A A T T G T C T T T G T G A T T T G T C C C C T T G C T G C T
WI-11709	105	T A T T C A G T T T G C	A G A A G C T T G C T T C A G T T T G C	T C A T T T C T C T A A T T T A C G G G A	A A T A T C A T C A C T C A T A T C A G G C A T G T T T A T A A A A T G A G A G A T T A T G T C C T T T T T G G C A T A C T T C A T C T T C T T C A G G A C A C A G A G A A G C T T G C T T C A G T T T G C T [A] G T C C C G T A A A A T T A G A A G A A T G A A T G G C C A G A T G G A T G G A A A A
WI-11710	103	C A C A G T C T C A	G C A C C T A G C C T C A G T C T C A	G T G T G G A G G A G G G A G G A G	T T A T A C C A T C A A C C T G T C C C A G C T T T C C A G C A C A A C A G C C A C A C T C T A G A C A G C C T T C A C T C C A G T C C A T T C T G G C A C C T A G C C T C A G T C T C A G T C T C A G T C C A C A C T C C C T C C C A C A C A C T C C T T C

WI-11715b	123 C T	AGGCTGGCTGC AGCTT	TCCCATCCTG TGGCT	AGAATGGAGCTGTTGGGGAGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGCTGGCTGCAGCTTTC/TJAGCCAC AGGATGGGACTGGGGAAGA
WI-11715a	49 A C AAA	GCACACAATG TAAACAGAC AAA	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGGAGGACATGCACACAATGTAAACAGACAAA/CJTGCAATTACAACCTG TGGTGTAAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCAGCCAC AGGATGGGACTGGGGAAGA
WI-11727	43 G C TCAACA	AACAATCCTT AAAACAACATA	CCTGTGGTTTG TGTTGCAG	CTGGATTTCTATACCTAACAAATCCTTAAACAACATATCAACA/GC/CTGCAACACAAAACCACAGGC AAAATGAAAAACAGATGCCCGACAGACAGCAACCCACCACATGGCACACAC
WI-11728	16 C G ---	ATCTGTGGTTT ATCGCTG	---	TTTTATTATCAAACTC/GC/CAATTCCATTTCAAAATGTAAAGTTATCATCAGCTCCCATCCACTTT CTCCATCTTCTATCTCTTTCCACCTACACTTCTCTCCCTACAAACCCGGGTTCCAAA
WI-11758	61 A G TCGCTG	GCCTCACAA GTATTTCTAA	TGATGGCOCT GTGGTCTA	TTTTCTCTCTTTTAAAGTCGCTATACTAACTAGAAAGGAGAACTCTGTGGTTTTCGCCCTG/GJTAG ACCACAGGGCCAATCACACAGCTTCTTGTAAGAAACATGGAGAGTGCCAAAGATCACCATCA
WI-11295	37 A G AATATA	GGCTCACAA GTATTTCTAA	AAAAGTGCTCA TCTGTGAACTC T	CCGGCTCACAAAGTATTTCTAAATATAATTTGCT/GJTAGAGTTCACAGATGAGCACATTTTCA CATTAGGTGATATGCAACAAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93 T C ---	GGCTCAGAGA GCAAGGAA	---	AGCATGATATTTCTGCCTGGAGTTTCTGTGAGCTCAGCAACAGCAGAGTCAGAGATTAAGAATT ATTTATGCTCTCTTTTTCCTCTT/CJTGATTTGTTAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42 C G	CCCAACTTACC AAACCTCTG	AAAACTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTATTTAATGGGCTCAGAGAGCAAGGAA/CJGACACAAAATTTACAGTCTGA GTTTTGCGCGCAGAGACCCCTCTCCACCTTTTCTATGCTGTGTACACACACACTGTGCCAAGCCTC AGA
WI-11790	28 A G	GCCTCAGAGA GCAAGGAA	CGGTAGGOGAG GCTAAGC	TAATTCACCAACTTACCAACCTCTGT/GJGCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAATGGCAAAATCATCTAACACAAAGC
WI-11879	61 C A AGTATACA	TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG/CJAGT GATTTCTCTCTTCTCTTTTATAAAGTGAAGAGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91 C T AAGTTTAA	GTTTTTAATGT GGTATTAGAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTACTAATTTCCCATTTCTCCCTTTTATAGTTTTTAAATGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATCTATTTCTA/CJTTGACAGCACAGTTCTTCAAAGTTTGCTATAGACAATCTGA AAATTGGGTTCTGAAT
WI-11906	52 A G ATCTGAA	TGTTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTTATAACATCAAAAGAAAGAAATCTGAAT/GJTGAGGGAACCTG CAGAAATTAACCTTCAGTCTAATTTCTCAGAAATGCCAGATGAAGATGAACCCCTTACAG

WI-11909	78 A G	TTTGTGTTGGG TGGTCAAG	CCTCTCTGAG ATTTCTGAAT AG	GCAGTTCTCTGAAAGACAAATGGATTGTGGAGCATACTGAAGACTATTCTCTAAATGGCTATTTGTGTTG GGTGGTCAAGTACGCTATTAGAAATCTCAGAGGAGGACAAATGATAGTGCAGCTGCAGCCAGCTCG GACTGGCTTGCAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCGAGTTCA/T/G/GTT TTATTAGTATATAAATGGCTTTACAGGAAGCATTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAACTTTGTCTGGAGAC/C/CCAGCTAGTCTAAGAAACTTCTCTAGGCTGAG CTCTCTGGGAATCTAAGATAAGAACTGAGATCTCTGGGAAGAGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTTT T G A T T T	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAGTACAACACTGCTTATTTTCTGTTGAAGATCAGATCTCTGGTTTATTTAA/T/ GIATCAACATTCCACCACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A	TGCCCTACTAC GCTTTTAAAA T A A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAAT/AJAATAAAATACTGTACACATTTCTCTCATTTCTCTTACGA ATACTTTCTTTTGTGATATTGCAATTTCTATGGCATACACAGAGGACCTCTCAATGCCCTG
WI-11049	85 C T	---	---	TTCTGCTGAAGATCACAAACAAATTTCAACCTCTGTGGTTTCAAAATAATTAAGGATCTTTGTACCTTT GTGTTTATTTCTGTTTCACTAAGGAC/TJAGACTTCAGAAAGCATAGTTCCTCTGTAAACGTTTTT AAACATCTTTTCAATTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69 C T	AAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGAAAGTTCTCACTCTGCACATATAAAAGGACAGCCAGATATCA AC/TJTTTACAGAAATGAAATAAGATGGAATAATTTTAAACAAATTG
WI-13654	49 A G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTGAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGT/A/GJGTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAGGTAACTTTTCCCATTTTACAGACAAACCCAGT
WI-11070b	135 C T	---	---	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAGAGGAGCTAGGACAAATTTCTTGCTT TCAAGTAAATTTGTGACTGAGCAGAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAAGTA C/C/TJGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAGGGAA
WI-11070a	110 G T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAGAGGAGCTAGGACAAATTTCTTGCTT TCAAGTAAATTTGTGACTGAGCAGAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAGGGAA
WI-12020	121 T C	---	---	AATCTTTTATATTTCCAGCTGTGAGACAGTATTTTGAAGGCTGATGTTACCTCTAGCGGGCAAACC AGAGCCAGCTATTAAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCATT/T/CJCTCTTTTAGC ACGTTCTTTGTTCTCTC

WI-11076b	142 G A ---			---	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGTGGCATCGGCTTATCTTCTTGGGAGGCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTGCATACCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTGCTAT G
WI-11076a	106 T C AGGCA	AAGGGGGAGC	TCCTGCTCTGG GTATGTGAC	GGTTATTCAAA AATTAGTATGG GACA	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGTGGCATCGGCTTATCTTCTTGGGAGGCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCAT/GTGCATACATACCCAGAGCAGGAGAGA GAGAAAGAGAGAGGAAGTCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTGCTAT G
WI-14263	49 T C GGCATATTCA	CGCAGAAAA	GGTATTCAAA AATTAGTATGG GACA	---	ACCTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA/TCTGTCCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA AATTATTGCTGAAATTAGGAAGGAGCAT/GTGAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAAGCAAGTACCATTTTCCAAAGTATAAACTCGTA
WI-14267	28 T C ---	CTTTTCATTT TGCTTTTAA	TGATGATGTCA TATACTAAAA ATCAAAAG	---	GATTTGTTTATTTCATCTCGCTTTTCTATTTTGTCTTTTAAATAGAACA[G/A]CTTTGATTTTGTAGTA TATGACATCATCATCATGAATTTTCTCTTCTTCTTGTATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-13892	50 G A TAGAAC	CATGAGAGGA	AAAAGCTTCTT TCCCTTGGGA	---	ACCTCTTCTGATGACACTTGTACCTGTAAAGGGTCTAGAGAGAAAGAGTAGTACTCTCTTGTG TACAAATTCAGGATGCGAGGCGCATGAGAGGATTCCTCTCTCTC/GTCCAGGAAAGAGCTTTTGGC AATAAATGGAAGAGGAGTGAACAAAGTAAATGAACAAACAGACCCAGATCAGAGGAAGAGATG GCTTCTTGTAAATTCCTGGAGCA[G/C]ATTCAAGCAGCAAAATATTTACTGAACACTTGTCTATGTGCTG G
WI-13951b	88 G C ---	GGAGTGAACA AAGTAATGAA CAAAA	TTCTCTGTATC TGGGGTCT	---	AATAAATGGAAGAGGAGTGAACAAAGTAAATGAACAAA[C/T]AGACCCAGATCAGAGGAAGAG ATGGCTTCTTGTAAATCTGGAGCAGATTCAAGCAGCAAAATATTTACTGAACACTTGTCTATGTGCTG G
WI-13951a	39 C T CAAAT	AAAAGGCTC TTGCCCAT	GGAGGGAGAG ACGGGAATA	---	GAGACCAAAAAGGCTCTGCCCATG/AJATTCCCGTCTCTCCCTCTGACTGACCCCACTGTCTT ACAAATGAACATCCCTCAGCCCATGGCATGGTGTGATCCCTCTCTTGGGATCTGTGAATATAACCA ACTGCTTGTCAATGGC
WI-13264	25 G A TTGCCAT	AGCAAAAAGGA AGTTAAATAC CTGATAGA	CATGAAAGGA CAAAATTTGCAT C	---	TTATTTGTCAATTAGCAAAAAGGAAGTTAAATCTGATAGA/CIGATGCAAAATTTGTCCCTTTCATGCA TTTGTGGAGCAAGTACTAATCTTGTCTACTGTCTATTTCCCTCACAAGGAGTTGAGCCCTAGATGAC
WI-13960	39 A C TGATAGA	ATCTTATAACC AAGAAGCCTT CAG	CTCTGGCTCAG ACTTGTCT	---	AACCTTTTATTGTTAGTAGCCCAAGTACTTATGTCATCTTATAACCAAGAGCCCTTCAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATACACTTGTCTCAGGGTCCACCAGGAACCCAGGCTTGGCT
WI-15843	62 C T CAG			---	

WI-13983	52	G A	TCTCTCCACT CCTTAAACCT	CAATACTCTGT TAGCCACAGTGG	TTGTGTATCTGATTTCGGAAACATAGAAATCTCTCTCCACTCTCTAAACCTTG/AJCCACTGGGCTAA GAGAGTATTGTACAGAAATATGCACACTGACTTAACAGAAATTAGAACATOCAGGCACACTCACTGAGA
WI-13850	51	A G T T	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTAA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTAAACACAGCCAT/GJTTACAAACATTGT CAGGGAACATTACAAGAAATAAAGATGGACTTGCAGGTGTAAAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCTG	TGAATAGTTGG CAAAGGAAA	AGATGTCAAGTTCGAATGTATTCTCTGATG/CJTTTCCTTTGCCAACTATTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAGGCCCCGAAAATATGAGTGAGACTCA
WI-14284	55	C T ---	---	---	ATTTCAAACAAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA/CJTTTATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85	G C C C A G A T	CCGCTGCTATT CCAGAT	GGTCTCCTTC ACCAAATCTT	ATGACCAGACCAAGAACGCTGTTCTATATGAAGACAAACAGGTGGCCATACTTGGGTGGAGGGATA CCGCTGCTATTCCAGAT/GJAAAGATTGGTGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C T A C A A C	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTGATGTAGTTACCCCACTAATACAAC/CJTGAGAACCACTGACTTCAAATATTATGAGAG AAATTAATCTCAGGGAATTTTGCAGAGAAGATAATA
WI-13529	42	T C T T A C C A	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCATTCCACAACATTTATTGAACAGTTACCA/T/CJAAGCAAGAGAGTGAGAAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCTGAGGGGTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84	G A ---	---	---	TTATTTGTCAGAAATTCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAGTTTACTAC TTTGAAAAAGGAAACTAT/GAJACAAACAAGTATATATTCAGGAAAGGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C ---	---	---	TGAAAGGATACAGAAAAAAGTACGGAAGT/CJGAAAAGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAAGCTTCCAGTTGCTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G A ---	---	---	TTTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAAATAACATCTCAC/GJAACTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTCCTTTGACGCCGGCCCTTGAATCTGACATTCAAGTCAAC CGTAATAGAAACCCAGAGCT
WI-13477b	61	A G ---	---	---	TTGGTTTTTAATACCTCTGTTGGATAAAAGGACATTTGTTTTCATTAGCTTGTCTTCAAA/GJGAC AGAGAAAATAAGATAAAATACCTTAAAGAAATTAATAGAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A G A G G	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTGTTGGATAAAAGG/GJGATGTTTTCATTAGCTTGTCTTCAAAAGAC AGAGAAAATAAGATAAAATACCTTAAAGAAATTAATAGAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACTTTATTAGCATGCAATGCAATTTATTCTGGCAATAAATTAAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAG[AT/JAAAATGTTTCTGTAATGTGCACACTAGAAATATATGCAGAATCCTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAA	TCCATGTAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAGAAATCAACA TGTGCACAAAAGAGTAAATTT/GJACCAAAAATTAAGATTTTTTGGGACAATTCACATGTTG AAAA
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGGA[CA/JTGGAATCTAACTGCGCAGAG AAATCAAGACCGATGGTGAAATCTGGGCAGCTTCAAAATTTCTGCCTCCTTAAACATTTTCAG CCAAATTTTCATTATTGCC
WI-13857	28 A G ---	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC[AG/JTACATTTTAGGTATCTGGCACAATTAACCAATGT CTGCCCATTTTGTGTAGCTTTCATACAGTACAGATTTTCATTGATGTCGCTCCACATCTG
WI-15809	77 T G	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAAA	GTTTAAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC[GT/JTTTACAAACATTGAATTAGTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T ---	---	---	TTAATCAGTCTGTGTCAAGAAGAACAGGACTTGATCAAGCTTCCAGCCCTCACCCTCTATCAGCA TAGCAATTTTAAAGGATCAGAGCTTTGTTTACATTTGTCTAAAACCAAGAGAGAA[AT/JGGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCCTTTATTCCAAAGATGGGAAGCGCATTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACTA GCTGCAGTAAATAC[GT/GJGATCCCATCCACTCTTCTCTTTTGTGACTGAAACTCTTCAAGAACT GCTGAATGCTCTCTCTC
WI-15801a	24 G A	TTTATCCAAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCCTTTATTCCAAAGATGGGAAGCG[AG/JCATTTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAAATACTGCATCCCATCCACTCTTCTCTTTTGTGACTGAAACTCTTCAAGAACT GCTGAATGCTCTCTCTC
WI-13763	59 T C	GGCTGGACACT GCAGTGAT	CCACACCTGC CCCT	GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGATTT/CJAGGG GCAGGTGTGGGCGAGGTGGGCTCTGAGCGAGGACAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48 T A AACC	TCAATAAAGA GCAGAAAAGAA	CAGTGTGAAG AACATCTTTT GTC	TTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAACCTT/AJAGACAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTGATATTTTGTCTTTTCCCGAGGGCAAAAAGA GAGTCTTCCAGAAACCTC
WI-13789	62 G A	TTGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTTC	TCCAAGGAAAAGAAAACCAATCAGTGAGAAAACCTCAAGAAATTGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGCTGGGACTGGAATATGGACAGTGGATGGTAGGGTCTCACTCTCTT GAGGTCCCT
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCTTTGGCCA GTACTTTT	AATAACAAGTTTAAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACAGATCACAAAAAGC[G/ATGCACAAAAAGTACTGGCGCAAGGACAAAATAATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15825	40 C T	---	---	GTTCCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[C/T]TGTCCTCATATAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACACTGAA GACTCACCGAG	TCCCCACCCCCA COCT	GTCTCAGTTCTTGCTAGGCCTGTAATTTTCAAGTTTAAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCGAA[C/G]AGGGTGGGGTGGGAATACCTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCCT
WI-13600	26 G T	TTAATGAGCC AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCAGTTTAAATGAGCCCAAGCATCCAT[G/T]CCATCATCTAGTAACAAATTTTCAATATGCACATTATAT TATACTGGAACAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCAATCAGCAACCCCTCT TGATTCCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATATTTA ATATTAAT	GATAGGAAAAAGAAAGAAATGAAGTCAATAGTCTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC CTTTCCATTCTGGAGACAACACAC[A/G/T]AATCTATTAAATATTGTCATGAGGTATGCACCT GCCCC
WI-13650	76 A T	AAAGATTAC AATATTTCACT TTTAAAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAAACATTTAAAAATTTCTGAGGGATATTGATGAGAACTATGATGAAGATTCAACAATTTTCAC TTTTAAAAAC[A/T]TAAAAAACTACTCTTCATATCTAGCCTGATGACTTAAAAAGTTACCGG
WI-14319	83 C T A	CAATTCGAAG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAATT
WI-13528	80 A G A A A	CAATACATTT GCATTTTCCTA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAATCAATACATTTTGCATTTTCTTAAAA AAAGAAGACATTT[A/G]TTTCAAGAAAACTGTGGTATCATGCAAGAAAAAGCAGAAAAAAAT
WI-13909c	93 A T	---	---	ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCACAGTGAAGTTTCTTCTCAGACT CTCTTCAAACTCG[A]AATATCTTTTCAGAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A	TTCTCACACT CTCTTCAAACT GAC	GCAGTGGGTAC TAGCTAGACAT CTC	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAAACAAATTTATAAAGGGACAGAAAAATTAAG AATCAAAACATCATCTCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-14323a	78 T C	ACAGAAAAAT TAAGAATCAA ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAAACAAATTTATAAAGGGACAGAAAAATTAAG AATCAAAACATCA[T/C]TCTGGACCATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-15389b	104 G A A A	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCACACTT	AAAAATTGACAAATCAACTAGCTTCTTTTGTGTTTGGAAAGTACCATTTTCAAAATTTATTATGT AATACACTCATCCAGATAATGAACATCTCGGAAA[A/G/A]AGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33 G A TC	AATCAACTAG CTTGCTTTTG	TTGAATAATG GTAGCTTCCA AA	AAAATTGACAAATCAACTAGCTTGTCTTTTGTGCG/AJTITGGGAAGACTACCATTTATTCAAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTCGGAAAAGAAGTGTGGAAATCACCTCATCTGTGTC TGTAATCTGCTTACAGTCCTTTGCAAGACAGACATATGTTTTTGATAAAGATATAAATTGCTTCAT TTTAAACTAATTAGTGTCTT/CJTJTTAAATTATATGAACCTTTTGGTGAATTATGAACGTGTACCAAAC C
WI-15747	88 T C AGTGTTT		CATAATTCACC AAAAGTTTCATA TAATTT	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTCTCTCGTTAAGTCTGGATATACCTTGGCTTGCAC/CJTGACACCTTTTACG GAGGGATTCGGACAAC
WI-13752b	117 CT ---		---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTCTCTCGTTAAGTCTGGATATACCTTGGCTTGCAC/CJTGACACCTTTTACG GAGGGATTCGGACAAC
WI-13752a	106 T C AGTGCTGA	CCTTCTCGTTA AGTGCTGA	CCCTCCGTAAA AGGTGTC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTCTCTCGTTAAGTCTGGATATACCTTGGCTTGCAC/CJTGACACCTTTTACG GAGGGATTCGGACAAC
WI-14339	102 T G TTAC	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAATTTCACTGGGATGGAAG CAGATGAACCCACCAATCAACACAGTACATGATTACT/GICGGTTTCCAGAAATCTGGATAC TGGATGGATGGATGAGGCCACCTGTGTTCACAAAACACGTAATGGAACCTTCATGCAGCTTAGAT TTCCCTTGGCCAGCTAGGAGCTTGTGTATGGTGTGAAACAACTGAAC/CJTGCTGTGCTTATCTTTC CTGATCT
WI-13744	115 CT AAACTGAA	TGGTGCTGAAC AAACTGAA	GATAAGCACA GC	CCCTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAAGAGAGAGCCCCCGTACATACCTTAT IC/JAACCATTTCATCCACCATTTGTAAATCTCATCTTCTGGGCTGGATACTCAAAAACAGAT
WI-14061	68 CT ---		---	TTACAGTTGGATTAAACACTACCACTACCACTGAATATACTGAATTAACATTCAACCCCTTTCATCCATTGAG C/CJAAATTTAAACCTCTGGCCAAGTATCATGAACCTTACGAAGAGGAGATAAGAGATCTGATC
WI-15719	69 A C CATTGAGC	ACCTTTCATC CATTGAGC	TGATACTGGC AAGAGTTTTAA ATT	TAATCCATCAATCTAAATCAACATACATAGATCAAAACAGAAAGTACCACAGTATGCTTTATTTTGA GGTATTAATTGGTTCTCTAAATCGATACATCCAAAACCTT/CJAGTTAGCAGCAAGCATCAGTTCTTC
WI-13810	106 T C AACTT	CTCTAAATCG ATACATCCAA AACTT	GAACTGATGCT TGCTGCTAACT	GGATTTTATTCACATTAACTTGCACAG/GJTJTAGCAAAAAAATCAAAACATAAAACATAAGCCACA TATCAAGAACAATATACAATAGAGATTGAAATTTCTCAATAGCATTGGAAGGTATTTCCATAAATA TCAAACTGCACACTATAAAAGTGTCTTAAATGACAGCAGGAGATGTGAAGACACAAATGAAC AAGTGC/GJATAGTGACACATAGCTGTCAACACAGTG
WI-15736a	27 G T CACA	ATTTAATTCAC ATTAACCTTG	GTTCTTTGATA TGTTGGCTTAGT TTT	TCAAACTGCACACTATAAAAGTGTCTTAAATGACAGCAGGAGATGTGAAGACACAAATGAAC AAGTGC/GJATAGTGACACATAGCTGTCAACACAGTG
WI-13785d	72 G A ---		---	TCAAACTGCACACTATAAAAGTGTCTTAAATGACAGCAGGAGATGTGAAGACAG/CJCAAAATG AACAAGTGCCTAGTGACATAGCTGTCAACACAGTG
WI-13785c	56 A C ---		---	

WI-13785b	40 C G ---	---	---	TCAAACCTGCACACTATAAAAGTGCCTTTAAATGCAGCAG/C/GJAGGAGATGTGAAGACACAAATG AACAAAGTCGCTAGTGACACATAGCTGTCAACAACACAGTG
WI-13785a	27 T C TGCTT	TGTTGTGACAG CTATGTGTCAC T	---	TCAAACCTGCACACTATAAAAGTGCCTTT/CJAAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTCGCTAGTGACACATAGCTGTCAACAACACAGTG
WI-13793	88 C G ATAGG	GGGCAGGAGGA TTTGTACT	---	AGAAACCAAGTATATCATAGGCAATAAAATAGTTTTACCCCAATTGATACAACATAAGGGATTT TACATTACGCCTAGATATAGG/C/GJAGTAACAATCCTCCTGCCATAAATCTATGACTTG
WI-13794	52 A G TTCTTTCTC	AGAAATGGGCTC TTAACCTTGTA	---	TAGTCTCCTACAATTCCTTCAATCCATTTCTCCTCACCCCTTTCTTTCTC/CJ/GJACAAGGTTAAGA GCCCATCTTCAACAACAACAAAACACATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	---	TCATTTAAGTGCACTTTGAACCATGTGTAGACTGC/CJ/GJGGCACTTTAGAAAGAAAGCTGAGACTGAA AAGTCTGTCTTGACTTCAAGGAAGGGTAAGTCCCTGTTTGACGCCCGGGCTGCTCATTTGTTA
WI-13424	66 G A C	TTTTCTCCCC AGGGTCTA	---	GTCCTTTGCACAAGTCTCCCAACTGGTTTGAGGTTTCCCTCTGAGGTTTTCACCCATTCTTC/CJ/GJ JTAGACCTGGGAGAAACACATGTGTAAAGTGCTCAGGACATGAGGCAGGCCGCTTCACAAGAT GCTGGCTAAGGGCTTC
WI-14065	29 T C AATT	CAAGCTGAATC TGGGATCTC	---	AACTGTCTTATAAAAGGTGAGAGGCAATTT/CJGAGATCCAGATTCAGCTTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAATTTCTGTCTGCTTTTAATCCTGAACATCTTGAAGCACGAA
WI-13446	22 G C TCACTCATCA	AAGGGAATCA AAATCAGAAG G	---	TGCCATGTTCTTCACTCATCA/CJ/CCTCTGATTTTGATTCCCTTCTGCTCTGTAAATTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTAGAAATCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTT CTGACTGCCTAAT
WI-13725	56 A C TGGGTGCC	OCTGCTGTCTC GGGC	---	TCACACAAGGCATTTGGAAATGTCACCTTACACATGTGTGAGCACATATGGGTGCC/CJ/GCCCCGAG ACAGCAGGATAAGTTTCACAAACTTGACCAGGCAGGTTAGAACGAAGCATGGTTCCAGGATG ---
WI-15702d	107 T C ---	---	---	CAAAATGTTTATGAAGAGACTCCGAACAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCCTGTAAACAAT/CJ/ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101 T C ---	---	---	CAATGTTTATGAAGAGACTCCGAACAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCCTGTAAACAAT/CJ/ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90 C T ---	---	---	CAATGTTTATGAAGAGACTCCGAACAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCCTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA

§

WI-15702a	48 G C A A A G	A A C A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A T G T T T A T G A G A G A C T C C G A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G G T A A A G G G G T G A G G A A G C A T G T G A G A G A A A C T G T A C C C T G T A A C A A T A C T A A T G G G T C T T T G A A C A A T A G T T T T G A
WI-13831b	113 T C ---		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A G C G A A G G T G A C T T G G A A A G G A G A T T C A C A T A C T C C A C T G T A T C C T C C G G T A A G T T T C C T T C T C T G T A G A T C G T C T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	58 G C ---		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T T C C A C T G T A T C C T C C G G T A A G T T T C C T T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13806	62 G A ---		---	T G A T T G A G C T T A G A A G G A A G T C A T G T T G A A T C A G A G A G A G G C C A A A C T A G G C T C A G G T [G/A] C C C A T T A A G C A T G C T G T A A T G C A A A G G A A A A G C T T A A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86 A G ---		---	C A C A T T T C A G C A A C A A A T G G A G G T G C A A C A G G G T T A T T C A C A T T A A T A T A A C T G G A T T T T T T G T C A A A T A A T A G G A [A/G] T C T C T T A A T A A C C A T C C T C A C T T C A T G C C C A G T
WI-14373	95 A G ---		---	A G G C T G T T T T T G A G G C C T G A G G C C C C A C A C A T G A C A C G T A A G A C T G T A A C C A T G G T C A T G T G A G T T A T G A C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C C A C G C C T T T A C T T T C A C A G C C T C T G C A
WI-14078	61 C T G C A A G A	A A A G A A G T A A A T T A G G A A G A	T G T G T C A T G T C T C T T A C T G C	A G A A C C G A G A A C T C A A A G A A C C A C A C A T G T G T A T C A A A G A A T A A T A G G A A G A C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A C A A G G G C A T G G A A G A G A C T T A G A T G G T C A C G
WI-14083	47 C T A C A C T	A G A C T T G A G A G C T T A A A A C A	G C T A C T G G A C C T C T A A A C T A C T G A	T T G C T A C A T A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A C A C A C T C T A T T T G T T A T T T C A C A G C T C A G T A G T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T A G G T C T T A A G G C C A A
WI-14085	31 A G A G A A A A	C A T T T A T T T C A T G T G T A A G A	C A G T C A T G T T C A C G T C T A G T T	T G C A T T T A T T T C A T G T G T A A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A C A A A A T A G C A T G T T G A T T A A G T G A A A T A C A G A A C A G G A G G C C T T T
WI-12169	121 G C T T G C T T	A A T A A A A C T T C C T A T T T C T T	G G G T C T G A G G T G A A A G A A A A	G T C A A A G G T T G C A A A T T T A T T T C A C T T A T C A A G A C T T A C A A A T A T T T T G T T C A T T C T A A A T T T T C A C C T T A T T G C T A A G T T A T A A A A T A A A A C T T C C T A T T T C T T T G C T T [G/C] T T T T T C T T T C A C C T C A G A A C C C C C T T A
WI-15705	50 A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G A G A A T G A A G G A G G A G A T T T A G A C T G A A T C [A/G] T T C T A G A G A T T T G A C G A C T A C A G C T C T C T C T C T T T G T A C T A C G G A C C C T G C T T A T A G C C C C A C A G A A A T C C T C A T C T C G G G T T G C A G A C A G

WI-14379	102 C T	TCTATTAAACA GGGTTATGTCA CACC	ATCATCTGTTT TGAGGTTGACA ---	TTTATGCTGTTGTTTCTACTGCTGGTGCTGCTCAGTAAATATCCAACTCTAGTATGATTTTCTTT TACTTGCTCTATTAAACAGGGTTATGTACACC[C]/TGTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA[C]/A/C/CACCACTTAAACAGAGGACACTGCAGAGGCTTATGTACA ACAGTGTCCCGGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22 C A	CGCAGAGCTG CTGTATTTAA A	GCAGAGATCCA GACGCTTGT	ACCGCAGAGCTGCTGATTTTAAAGACGCTCTGCTGATCTCTGAGGGGCTGGACCAGCTGC AGTGGGGCTCGGCACTGCTCTGCTCTCAGGACTCTTCCACCAACCC
WI-15937	24 A G A	AACTGAAAC GTATTTCTCC	GGCCTTTAAGT TTCTACGGTG	TGAAACTGAAACGATTTCTCTCCA/CACACCGTAGAACTTAAAGCGCGCAAAAGACTCACACCC ACCACCTAGCGCGCAAAAAGGAAGTTTCAGGTGATACAGATGTCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24 A C A			ATGTTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAATAATCAT ATTTAAGTCCCGTTAACACTAAGCC[AGT]ATTATTCAAAATGTGTTTCAAAATAGTCAGCCAGAT CACCAAGCTCAGTCACTAC
WI-14124	92 A G			GACAAAAGGCGAGTTTCTGTAGTTTCCAGCAGGGCCAGAGCAGTATCAGAACGGGTGTTTGACCT GCATAGATTTTTGACGACTA/C/TGTGCCATGCCATTCTGTAGTGAAATTAATGAACA
WI-14125	88 C T	GGTTGACCTG CATAGATTTT	GGATGGCATG GCCAC	GTTTATTTCTCACAGTTCTGGAGTTAGAACTGAGTCTGAGATGAGGATATCACCAGCATGGTTAGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGTTCTCACCATGTCTTCACATGAG/C/GCCCCAAAGAGAC AGAACAGCTCTCTGGT
WI-14136	120 G A	ATGCTTCACA	CAGTATGTACA GTGACATAACA	TTGTTGTTGGCACCAGAAAAGCTC/TATGTTCTATGTTATGTCACCTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTCAATG
WI-14138	23 C T	TGTTGGCACC GAAAGCT	TAGAAC	GGCAGGTTTATTCATAAATTTTCAAACTTGAAGCAACCAAGATGCTCTCAGTAGTAGTATATTC GACAATC[G/A]AATATTACTTAGCAGCTAAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74 G A	GACAATC	TAATATT	TTTTTAAGAGTGCTTTCACATCATTTATATTGATTTGCACACAAAACTTTTTAACTC[C]/TGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGATAGAGCCCTTCTTCAGAATCA CCTCCG
WI-15953b	59 C T			TTTTTAAGAGTGCTTTCACATCATTTATATTGATTTGCACACAAAACTTTTTAACTCCGTC AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGATAGAGCCCTTCTTCAGAATCA CCTCCG
WI-15953a	26 T G A T	TTTTAAGAGTG TCTTCACATC	TCATCTGTTCT TGTTGTTTTTG A	TTTTTAAGAGTGCTTTCACATCATTTATATTGATTTGCACACAAAACTTTTTAACTCCGTC AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGATAGAGCCCTTCTTCAGAATCA CCTCCG

WI-14631	82 G A ---			---	TGAATTCATGGACAGTTTGCCTCTGTTTATGTGAAACCCCTCACAAGCACTCTGCATAGTCCGCTTT CTGCTCTTTAAACG/AJTGCTGGTCCCTCTGCCCAAACITTTAGGATTGGCCTCCTCAGGGCCTT GTCTGA
WI-6053	24 A G ---			---	ATCACACCGTGTCTAAGAACAAC/AJGTCCTCATGTCCAACTCATATCCCCGGGACTTTGTCAACTG CAGTACACTTCTCTGCATTGAACCTGGCTTCTCTGGAGGAAGCCTCTAGAGCCAGGTAAGGGGTGC AGCAGTGAGGGGTATATCTGGGCTGGCCAGTTGGAACCAAGGAG
WI-15964	99 T A CTGGAGGTA	GCTCTCTGTCC		GACTTCTCCAC CCTCTTGC	CAGAAACCTCTTCTGTGTATTAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGGCTGCCTT GGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTAT/AJGCAAGAGGGTGGAGAAGTCTTTGGCAAG
WI-12075	103 G A GGCAC	AGCAGCTGGG		CCCCCTCTTTC TCTTCTCTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAGCCAGGCAAAATACCCATCAG AGACAGTGACAAGAGCAGCTGGGGGCACGGGGAGGC/G/AJGAAGGAAGAGAAAGGGGAGGAG CCT
WI-12179	96 G A TGGAGGTCA	GGAGGTACGG		TGGAATGACCC TGTAGATGC	TAATTTAAAAACACGCCCTTCCCACATAGTCGTGAGGCATCTGCACATTTTCTAGAAGGACATGA ATAGTGATGTGGAGGTACGGTGGAGGTCA/G/AJGCACTCTACAGGGTCACTTCGAGGAGGAACAG
WI-14651	49 C G ATTGT	CAAGAATCAT TCTCATTTAA		GGAGATATTGA TCTTTTCTGA CTTATTT	CACAAATAGTGAATATCTGAGCAAGAAATCTCTCATTTAAAATTGT/C/GJAAATAAGTCAGAA AAAGATCAATATCTCCCTGCTTCAAAATGACACTCCCAATTTTCACAGGTAAACCCTGTTA
WI-14666	105 T A ---			---	AATGTGGACTTCAACAAGGGTTTAAACCTAATCTAATACAACCTCTACAACACATTCAGAGCAT TATAACAAGAATTATTACAGGCAGCTAATGTATTAAAT/AJAACCATGAAAAAGAAAAAACTTG
WI-13473	31 C T ---			---	ATCTAGATGTCAGCAAATGGGCTGAGACTGT/CJTTGTCTGCTAGATGCAGTGTTTGTATGTTTCTAC TCTATTACAAAAATTAAACAGAAATATGGCTTCGCTTTGTGCAATGTTTATATCACAGTC
WI-13967	103 A C AAATAAAAA	AAAGACTAC AGATACAAGG		TTGTGTTTTCA TCTCCTAAAAG TG	AATTTAATAGCAGCTCTGTGTTGTGATTTTAAAGAACAAGATAAAATATGTCAATTCAGCAGTCATTT AAAAAATAAAGACTACAGATACAGGAAATAAAAA/AJCACITTTAGGAGATGAAAAACACAAA
WI-14408	60 T A G	GCAGACACAC TATTACAGGCT		TAAATTGTGA AAACTCATTTG TTACTTT	TTAATATTCAGCAAAGTTATTGCAACAGGTGAAAATGCAGACACACTATTACAGGCTGT/AJAAA GTAACAAATGAGTTTTACACAATTAAATATTACACATACTATGGGATTTGTTGAATGA
WI-13683	47 C G ---			---	TTTTGTGTTAAGAACAGCATTTTGAAAAATAAAACCTATCTGCCCATG/C/GJTTTACAGCCTTTTAAAT TTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63 C T CGTCT	CACCATGGCA		CATTGAGATAA AGCACACTTAT CAG	TTAGAAAACGTATAAAAGCAACACAACCTTTTGGGAAAGCACCATGGCACGTCCTTTGTGCTA/C/T GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22 G A ---			---	ACATGGCAGATACAGAGCTGT/C/GJCTCTTGAAGACCACCACCTGACCAAGGAAATGCCACTTTTACAA AATCATCCCCCTTTTCATGATTGGAACAGTTTTCTCGACCGTCTGGAGCGTTGAAGGGTGAACGAGC

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WI-16002	59 T C	GATAACATAA AATGATCATG AGAATTC	GCCATCTCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTCATTCGTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGGCT
WI-15381b	101 A G A	CCCACTTGAAC TCAAGTCATC	AAACTAAAC CTTTGTGCTA AAA	GTGGAATTTTATTAAGCCATCAAAATTTCTTCACACTCACTACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAACCTCAAGTCATCAAGTJTTTAGGCACAAAGGTTTAGTTTCTCGG GAAATCAAGTTTAAACCA
WI-14759	73 T C	GCGTTTGACTT GTGGGG	TCCACACTGC OCCC	TGAGTTACAACAATGAGCAACAAGTTAGAAAAATGGTTTTTATTCAACTTCTAGCGTTTGACTT GTGGGGTTCGTACTCAATGGGGGCGAGTGTGGACGGGAGGATTGCAACAGAGTTTCATACTG CAA
WI-12535	50 A T T A T	CTAGGAGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTCAGGTGTGACTAGGAGGTTGAGGTGTAGATATATJCTTCTCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCGTTCTTGTTTATCAGCTGAGAGGGCAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112 G A G G G G A	AAAGGCACAC G G G G A	CTCAGCCTGCG TTGACC	TTCCATTCTATGCTTGGCTTACCAATTTTATAGCTATTGGGAGGCAGGAAAGGAAATTTTGGC CCAGAAACCATGAGATTTGGTCAGAAAGGCACACGGGAAG/GAGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18 T C		---	ACACAATATAATCCATTC/CJCGAGTGATTAACCTATTTGTTTGTAGAACCAACAAACTAC AAGAAACATTTCAAAACCTTTTTTTCAGGCTGA
WI-14808	52 T A C T A C C C T G T	ACCCACCACA CTACCCCTGT	GAGGCATACA ATGTTAAGATT TT	CTTTGAAACACTTTAAGCAACAGTTAAAAGTACCCACCACACTACCCTGTT/AJAAAATCTTAAC ATTGTGATGCCTCTGCATCAATTTTAGAAAAACAAGAAACACAACTGAAGGCCCATGTA
WI-14816	29 A T		---	AGTTAAAAAATCGAGTCAGCATTTATTAJAAAAAAGTGGACACGCTTCTATAATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
WI-12542c	71 G T		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTTAGATC ATG/GTTAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G T		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTTAGATC ATG/GTTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C T	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTTCTATCCATGTGAGGGCTTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C T	GGATACAGCA GTAAAGAATA CAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATTTCTAGAAACTGGGGATACAGCAGTAAAGATAACAAAAATCCTGCCTCTTATA GAGCATACATTTCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28 T C ---	---	TC TTG GGG GATAGAGGACAGAGTGTTTCJGTTGATTTTCGTTTCGGTTTCAGTTTGGTTGTCATT GGTTTTGTTTTTGCTAATTTTGCCCAACCTTATAAAAGCAGTGCACCCAGAGGCAG
WI-14856	60 A T A A	TTTGTGCTA CTTTTACAAA CTTT	ACATTTCTTATGATAGCAACTAAATATGATGGTGTGACACGGAAATACTTAATATTTAA AGTTTGTAAGAGTAGCAACAAAATGAGTATATCTATAAGTGATAGAGGATGTATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14863	61 G A ---	---	ATGGCAATTACTTTATAGCAATGAACAAATATTTGTCAAAGGGCAATATTTTGTGCTG/AJAG TTAATAAGTTAATATCTTTACCACAAAGCTAGAGGTCAACAGTACCCTATTATTGATTGCCACT ACCTGGC
WI-14867	46 T C A	TGGGGCTGCAG ACATC	TTTTAATTAACGTA AAAAGGCGAGCATTTCCAGGCTCTCTAACA/T/CJGAGTGTCTGCAGCCCCA TTGCTTTGAGATGTGAATGTGTTAACCCAGGTGGA
WI-14733	98 G A A	GATGAGGTGAG GCCATTATT	ACGGAGTCGTCTCTGATGTATTCTTGTCAAAAAATGTTTGCCTGATTCTAATCATGAAAGACAATT AGAAAAAATCCAAATTGACAGATATTCTGCA/G/AJAATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79 A C ---	---	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/CJAGGTGCCACTAAGGAAA ACTTCTCCAT/CJAAGCTGCTGTGTGCACGTTGCCTGGCTTTGCTAACCCCTGGTGTGCATCT GCCTGTGTTCTGTCTT
WI-14898a	50 A C A	AAGTTTTCCTT AGTGGCACT	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/CJAGGTGCCACTAAGG AAACCTTCTCCATAAAGCTGCTGTGCACGTTGCCTGGCTTTGCTAACCCCTGGTGTGCATC TGCTGTGTTCTGTCTT
WI-14907	48 G A GGACTCTGAC	TCGTGCTGCAAG GGGAAT	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC/G/AJATCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGCACACACCCATCAATCAGTGAATCTGCTGACGAGGGGCCACATG CAGCATGCTCACGTGTG
WI-14911	52 G A C	CAAACAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAGCTCAGTGCACCAATACATTAGTCTGTC/G/AJAGGTCCCTTTTC CTGGTTGCAGACAGATACCTTGTCTGATCTCCTCAGATGGCAGAGAAAGAGAGTAATCT
WI-14913	88 C A ---	---	CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGCCAATTTC TAGTGATAGTAGGAGACTCA/CJACTGACGTCACCTTTTCATATACAGATCAACCAATCCAAAAAC CTACACCTCCAACCACT
WI-14914	66 G C A	CAAGCCAGGA CAATAAATTC	ATTTCTTGTGCTGTGTAAGCCCTGTGAAGTCAATGCACATCTGGACACAGTTTTTCTCTAGCA/G/ CJGAATTTATTGCTCTGGCTGTGATGGCTTTCACAGC
WI-14926	49 T C ---	---	GTTTATTTTCAAAATGACACATCCAGATTGAAATGGGCACCTTAGCGAA/T/CJACTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAGACAGTTTTCAAAATAAAAAATTTTCTTAATCAGGTCCA

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WI-16083	89	CT	ATGTTAACA CAAACATATC AAGGAT	TGGAAGATT CCAGCCC	GCATCTTTATTACACAGAAACTCATTATGTCCTTAATCATTTGTTAATATATATATAAGCATGTT TAACACAAACATATCAAGGATTC/TGGGCTGGAATCTTTTCCATTCTATAGAAAAGCACTAACCATC CATTAAGCAG
WI-14930	55	CT	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGATTC/TGGGGTATTG GTTGGTTGTGTTGATTGGGAGACAGGAGGAGCAA
WI-14946	47	TC	---	---	TCAATCTGAAGGTGTCAAAGTGGTCTATTGGCCCAAGACATAACA/TCTCTAAATCATCTCTCTA GATCAGGGAGTCATAAGGACCATTAAGGCTCATTAACACAGTACTTTATGGAAAGGATT
WI-15987b	80	AG	---	---	ACATTAAACAGCACAAATTAAGGGTCCCAACGAGGTGGTAGTGGCTTCCACTATGTGAGGACAC TAAGAAGATGGTCA/GTCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32	CT	CACAATTAA GGGGTCCAA	GGAAGGCACTA CCAACCTC	ACATTAAACAGCACAAATTAAGGGTCCCAAC/TGAGGTGGTAGTGGCTTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56	TC	AGGGAACCTG CTAACTTGTC	GATGATCTTAC ATCAGTTGTTG GA	GAATAAGTTCTTATTGCCGTTCTTCAGGGAACAGGGAACCTGCTAACTTGTCAATCTCTCAACA ACTGATGTAAGATCATCTCTGACCATAGCAACCTGTGAAGGTTGCTGTTCCTCCAGCTGA
WI-16100	52	AG	CAAAAGCTA TTTCTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGACATG/GJGTAATATACTG TTTTCTGACATTCCTGTTATCAACTCCTCTGAAAATC
WI-14958	83	AG	AATAATTTAT CTCTTCTTTT CAAGGG	AATGCATTCTAT TTGGGTTTTT	GTGATTGATCTGTAATATTGGGATTATTTATCAACTCTAAAATCCAAAGATGAAAATAATTTATCT CTTTCTTTTCAAGGG/AGJAAAAACCCAAATGAATGCAATTTTCCAGGCTTTTGAACCTGC AGCAGAAAAATCAAGGA
WI-14976	35	CT	GTTGATTGCT TCGTTCAAAG	TCAAACATAAT CTTCCATTCTA AGC	TATTTTATTAAATGGTGGTGGTTCGTTCTCAAGGCTGCTAGATGGAAGATTTAGTTGAGGAG GGCAGGTTTGGGGTAGGCTCAGCGGCATAGTGGCCACAAAGATGCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31	GT	TCAGTGGTGT TATTGGATTTT	CACCTCTGACA TAATACCTTAGC ATAAA	TAATTGATTCAGTGGTGGTATTGGGATTTTGGTTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80	CT	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCTCT	TGATTACATTTTAAATCATGCTACAGCCCATCTAAGCCAAATTCAAAACACCACCTCTGCATTA AATGAAGCTGCAG/CTJAGGAAAGCTGAGCACATAGCACCCAACTGATCGGAAAGAAACGTA
WI-15002	72	TA	---	---	AAATCTCTTCTTCACACACAGATGAACCTTAAATAATACAAATGCACCTGAAAATGCCTTCTTGA TTTCCT/ATTCAGTTTAGGCTCAAATGGGCTCTCTCAAGGCTGGACCTCAAAGGCCAGTT
WI-15000	90	GA	GACAGAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAACAGATGGATAGACAG AAAAAGACTCAGACTGCTAAGTA/G/ATGAAGTTTGTGCAGAACTAGAAAACAAAAATCCACCT

WI-12323	68 G A	CACAATACTT CATGTACCTAT GAAATAA	CACTGGACATA TTCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACACAATACCTTTCATGTACCTATGAAATAA G/AJACAGGTAGGGAATATGTCAGTGCAAAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91 A T	AAGGGACGAT TTAGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTATTACACGTCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAAAACA/A/TJCAAAAAAACACTGGACATGCCCTGAAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100 C A T	CCTGCCTTTAT ATTGGAATTTT T	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTAGCACCTGAAATTTAGGCAAGAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAATTCCTGCCCTTATATTGGAATTTCTA/C/AJAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGCACTCAGCCCTTC
WI-14712	38 T A CA	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGTATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAAGTACAAATCA/T/AJCTCACAATACCATATACAACTACT TTCAATCACAACCTCAAAATATAAAATAACCTACAAAAATCACATTGC
WI-13712	40 A C TCTATTG	TTTACTTTGTT GTCAATTTTAT TCTATTG	CCATAAGGTCT CACACTTTTCT TAT	TGGGATACCCCTTTACTTTGTTGTCATTTTATTCTATTG/AJCTTATAAGAAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGCAATATGCAATATAATATTGTGTTGTTAAATTTATGCAAT
WI-16163	35 C T A	TCTGTTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTACTCTGGTGATGCAATTGAAATAA/C/TJATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAAGTTTAAGAGGACTATTCTTTAAACAAGACAGTGTCTGACATTTATTTTCAGGT
WI-13453	88 T A TC	AATGCACAAA ATCTTGTCTCT TC	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTGTCATTGAGTGTCTTATTATATTGGAAATTCAGTGATATAAACATTTGTACAAAT GCACAAAATCTGTCTCTT/AJTGCTAGAAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACTCATTGTCCAT
WI-16167	58 T C GATTTT	CGCACTCTAA ATTAGAGATA T	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATTT/CJCATCTT ATTCACCACGAGCACACACACGACAGTAGAACAGTTCACACCTGATATAAATGCACAAGATG
WI-14482	17 G A ---		---	GCAGAACCAATTAATAA/G/AJATCTGCAAGTTJTCGCCAAGAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGATAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81 T C ---		---	TGTAGTTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATCTATGTGATTCCAGTATCATGTAC GCACATAAAAAAAT/CJGTGTGCTTGTCTGCTGTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97 A C CCCAGAGTCGC	TGAAGATTAA CCCAGAGTCGC T	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAAGTATACAGAACTCTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTACCCAGAGTCGC/AJCTCTCTTCAAAATGCACACAATTAAGACG
WI-15012	59 G T ATGT	GCAGCAAGAT TACATCAGTA T	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATAATACAGCTTTTTTTCATTGAAGCTTTG/TJACCT TACTATACTCTAGGCTATTGGAGTGTTCCTCCAC

WI-15100	74 G A ---			---	TCATTACAGCCAAAGAAAATACCCAAATTATTTCCAAATAAAGCAAAAATTGGAACAGACTGGA GTGAGAACTGAGTCCACCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGTTCTGGGGT GCATTCTAGTGGACTTAT
WI-14492	92 A T AATTACT	CCATTATTTTC CCAAATATAA		GTCAACATGTT ATATTTTCTTT TAAGAC	TGGTACAGAATGTTTAATTACAGAGGGCAGTGATTCAGTTAAATAAAATTAATAAAACCTTTATTTT CCCAATATAAAATTAATAAATTAATGTTCTTAAAGAAAATAAAGATGGTGACAGCTTT TCTTTAATTTTATCGGAATCCAGGACACAACAAGAAAACACCCAAAACCCACATGGAGACAGAAG ACGAGACACAACCTCTCCCGACCTGCGCTCTAGAGTGGGACAAAAGTGGGGTGGAGAC AG
WI-12002c	89 T C ---			---	TCCTTAATTTTATCGGAATCCAGGACACAACAAGAAAACACCCAAAACCCACATGGAGACAGAAG ACGAGACACAACCTCTCCCGACCTGCGCTCTAGAGTGGGACAAAAGTGGGGTGGAGAC AG
WI-12002b	68 G A ---			---	TCCTTAATTTTATCGGAATCCAGGACACAACAAGAAAACACCCAAAACCCACATGGAGACAG AAGACGAGACACAACCTCTCCCGACCTGCGCTCTAGAGTGGGACAAAAGTGGGGTGGAGAC AG
WI-12002a	30 C G GGACACAA	TCGGAATCCA GGAGCCCTA		TGGTTTTGGG TGTTTTTCTT	TTTTCAATTTTATTTCCAGAAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAATTAACCTTTG TTCTGGAATGGAGCCCTAGTTGCAGTAATGTTGTGCATAATAAATAATTCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-15116	96 C T GTTGCAGTAA			CCTGAATATGC AATTATTTATT ATGACA	GCAAAGCAAAGCTATGGAGGCCTAAAGGAATGGGAATGTTGTGTTGGTGGCTGCTGATGACTTGGT GCTTGTGTCATGGAGCAGAAGTCTCTGCTGCTAGAGGGCGTCACATATTTAACTGCACATAAT TTGGGCAAACCTGTCATTC
WI-12578	37 C T AATGGGAA	GGCCTAAAGG		TCAAGCGACCA CCAACAC	ATTTACCGTTGGCCCAAGATCTCCCTTATGTTGGCATTGCAAGAGACACTGCACCTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTACCATTTCCCTAA
WI-15153	40 A G GCATTGCA			T	CCTTTGTCTCTGAACTGGGACCAGGATGTGAAATAATTTTGAATCTGATGCGAGTGGATGGC TTTGAATCAAATGGG[GTGACTTTTCCCTGTTGGTGGAAAACCTCTGTGAGGGTTTGGCA
WI-15215	84 G C TCAAATGGG	TGGCTTTAGAA CTTGAGGAOCT AGAAAGCAAA		CCAACAGGGA AAAAGTCA	AGGAAAGAGTGTAAAGCAAAGGCGATCATTTGGATGGAATGATTATGTGTCAGGACACTTGAGGAC CTAGAAAGCAAAAC[GTGGAGTGATTATGCCAATCAAAATTCAGAGTTGGAGATATGCTAAA AATTGCTAGTGCAAAATGGACCCAGAATTGGAAGGGCTATGTAACACACA[GTATGTCACACCAC AGCATGTGAGTGTACAGATCCTCTTGTGCAATTCAGCTTTCTTAAAACACATCAAAGGCTGCA
WI-15152	51 G A ---			---	TGACTGTATACCAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[GTGCTGTTT GCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAACAGACATGCAAAACAGAGATAAAACACAAT
WI-15123	55 C T TAGGATG	TGTTAGTGACA GACAGATAAA		TTGCTTAAGGG CAAACAGAC	

WI-15182	49	C A	GCACAACCAG	GCATGGGTAA	GAGACTGCCCTGTGACACAACACTAGTAGTGACAAACCAGGGCAAAATAICAJTGTGGATTAAACCC
			GGCAAAATA	TCCAGCA	ATGCTAATGGGTACCTTTATTAGTAATCATGGTCCCTCATAGCATGGTCCAGATCCG
WI-15198	38	T C	GGGOCCTGGC	ACTTATCCGTC	GTGGACCTCTACAAGTACCATGGGCCCTTGGCACTATGTC/CJCTACTCTGCCTGACGGATAAGTTGGC
			ACTATG	AGGCAGAGTAG	ATATGGTTCAGATTGCTTGCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCTT
			CATTTATTGAG	GTGTAGTCTT	TCAAAGTGGTAAATAGCCATTATTAGTATCTTGCTTTGATT/CJGTCTACGTAAAGCATGTAAAGCT
WI-12601	42	T C	TATCTTGCTT	ACATGCTTACG	ACAACATTACGACCCTCTCTTCAAGAGGAAGTCTGGTATTATGGAAAAACATTTTGTGCATTCCAGAT
			TGAT	TAGAC	T
			TGGCAAAATA		
			TGCATAACAA	TTGAAAATGGT	ATGTTGAGAGTAATATGCCCTACATATTTAGTGAAGTACACCCCCAGATATTTTGGGGAGAAGAG
WI-14510	104	A T	AA	TAACTGGCA	TTGTTTGCCTTTTGTGGCAAAATATGCATAACAAAATATTTGGCCAGTTTAAACCATTTTCAAGAGT
			CATTTGCAAT		CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTTGCAATAAACACCATCATTT/CJCTGAG
			AAACACCATC	GGACCTTATCT	TCCACAGATAAGGTCCCGGAGAAGGGGCTTCCCTCTCTTCTGCTGGTTGACGTTCACGCGAGT
WI-15239	57	T C	A	GTGGACTCAGG	GAAGCCTTTTCTGGAATG
			GCATCATATG	GGACAAATGT	
			AACTGTCTAGC	AAACATAGCT	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACGTGTAGCAGTATTAT/CJGTATTAGCTA
WI-12634	52	T C	AGT	AATAGC	TGTTTACAATTTGCTCTGAAGGGGTCTAGATGTGTACACCCAGAAAGTGGTATTCTCTGA
			GGGCTTGACAC	GGAAAGCCAG	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTTT/CJTTGTTAAAAATCTCTGGCTTTCTCTGGCTGG
			AAAGTTCTAA	AGATTTTAAAC	TGAGGAGGCACAGGCTGGGCTTTCAGGTATCCACTGGTGCCCGCATCTGTTCCCTCCACTTCCCAG
WI-15249	34	T C	AAAGTTCTAA	AA	CCACATTTCTGGCTCT
			AAGACACCGT	CCCTCTCTCTCA	CTGTCCGGGGAAGACACCGTGCATAATGC/CJAAAGTGCACGTAGGAGAGGGGAGGCTGTGTGACTC
WI-12159	28	C T	GCAAATGC	GTGCACCTT	CCAAACCCCTCGAATATTTATGAATCTAAGAGTCCAGACGCAGTTTCATCCACGGAGATCTGC
				TTGCTACTAAA	
WI-12648	41	A G	CCTAGTGGCAT	AGTGGACATCC	TCCCAGATTGTATGGAATGCCCTAGTGGCATTAAGGATGC/CJGTAGGATGTCCACTTTTAGTAGC
			TAAGGATGC	T	AACCGATGTTAATTCACCTACTCCATGTTAGGTGCTTACTTGGATTATCTCACITTAACCAACACA
WI-12684	64	G T	CATGCTGTAA	GGAACAACAA	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC/CJ
			ACAGCTGTGC	AGCCTAAATGG	TCCATTTAGGCTTTGTTGTTCCATTAGAGAGCACAGGAGAGGAAATTTAGCATAATTTCTT
			AAAGGATGAA		TTTATAAGCTGAATGAAGAGGTGACACAGCGGACACTGTCTATAAGTGGAAACAAGGATGAAGCT
			GCTAATCATG	TCTCTCCAGGG	AATCATGGA/GA/GCAAGCTCCCTGAGAGACAGGGACAAATCAAGAATGAGCTGGAGAAATTA
WI-15260	75	G A	GA	AGCTTC	TCCTG
			CATGTGGCTGG	CCTTCCACCAT	AAGGTTAATGGACTCACAGTTCCATGTGGCTGGGAGGCT/CJTCACAATCATGGTGGAGGCAAAA
WI-15325	39	T C	GAGGC	GATTGTGA	GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
			AGTTGGCATTC		TATTTGAGTATTTTCATCCATGGCGCTTCTCACTCCCTATACATTCTCCAGGGTTGAGGTAGTCTACCC
			AATAGCCTAT	TGAAACTCCCA	CCATAGGTTCAGAACCTATGACCTGTATCTTCAGTTGGCATTCATAGCCTATC/CJTAACCTCCATGT
WI-13936	123	C T	C	CATGGAGTT	GGGAGTTTCATAATAA

WI-14528	62 T	TTTTAACTTT TCTGGATGGTA G TAAAT	CTCGATTAGCA CTTATTATAAA AATTAATAA	TATGCTTTATTGAAGAGAAATAGGCTATTATATATTTTAACTTTTCTGGATGGTATAAAAT[G]TT GAATTATAAATTTTAAATTTTATAAAGTGCTAATCGAGACATCACTGGGTATAAATTGA
WI-15347	74 C	GACTTCAAAG GAAAAGAACA T AATT	TCACCTCCCCA AGTCTTTG	TATTTCTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTCTCAAGAGACTTGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-14546	95 C	CCAATTTCTAG TGATAGTAGA GGACTCA	AAGGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCAATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTTCATATACAGATCA
WI-15353	37 G	TTTATTGGCTGTCTCTGTATACAATGTGGTGAACG[A]TCTTAATTCAGGACATCTCCACCTTG TTTTGGCTTCCAGTTGTACTGCAAGACCAGTGTGAGGCACATAGGCTGATTAAATCAGTGG
WI-14580	100 G	CATTTCCATCT GTCTTGCA	CCGACCAGAT CCCTCC	AGAAATTTTCTCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAAATAC CTAGTTATTATACACATTTCCCATCTGTCTTGCA[G/A]GGAGGATCTTGGTGGCTTAACA
WI-8540	73 T	GGCTGCAATT GGCTTA	GGCTTCTTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATGCGGCAACCACAGAAAAACACACAGCTACACAGGCCTGCATT TGGCTTA[T/C]GTGCTGAAAAAGAGGGCGGACCTCTTGATAAAGAATGCT
WI-8039b	97 T	AAGTAGAACACAAATAGATGGCTCAAAAATATCAGAAATGCACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGTT[C/JAAATATGTATGTGTCCGTGCATGTCAATTAATATCCTTCT TACCACAGTCACCTAAAGAACCAAGCTTAGGACTAGGACACAACTGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTTGAGATGATGATTTAATGCCCGCAGCCGACACCCACA
WI-8039a	87 T	AAGTAGAACACAAATAGATGGCTCAAAAATATCAGAAATGCACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGTT[C/JAAATATGTATGTGTCCGTGCATGTCAATTAATATCCTTCT TACCACAGTCACCTAAAGAACCAAGCTTAGGACTAGGACACAACTGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTTGAGATGATGATTTAATGCCCGCAGCCGACACCCACA
WI-8044	107 C	CACAACATTCAGAAAGTTTCTGCATTGTCTCTCTGATGTCTAAAAGATTGAGCTTTGACTAT ACGATTTCCACACACTGAACGCATTCATAAGTTTCTCC[C/JA]GATATGGATTCTCTGATGATTAATA AGCCCCGAATCTGGCTAAAGGCTTTCCACATTCAGACATTTGTAAAGTTTCTCOCAGTGTGGAC TCTCTGCTGTGTCACAAGAAATGGAATTCGGCTGAATGCTTTTCCACACT
WI-8550	32 G	GGGAACATCA ATGCAACAAG	TTTGTGGCTTG AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAACCTCAAGCCACAACTTAGTTA ATAATCATGGTTAAGGGACATTCGCAAGAGCACTGATGCCCTCAGTGAA
WI-8057	87 T	TATTAGATAAAACCCCTTGTCCGATTCAGGATGTTAATTTGCTTCTCTTTAACTCTGTGACTTTT CCTGGTTCAAAGGACAGT[A]GATGGACAGCAGCAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACTCTGTGGCTCACAACCTGCCCCCTGTGAGAGGATGCTGCCCTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTTTGAAGCAGCCAGATGGTAAGG

WI-6192	91	A G G A T	G A C T G C T A A G G A T T T A A T T T G	T G A A G T G T T A G A T G G C T A A G T A T T A A A A	A A G A G A C A A A T T A G C T C A G T C C A A C A T G A T T G G C A G T T G G C A T A T T C T A G T G A A G C A A G T G T T C T G A C T G C T A A G G A T T A A T T T G G A T T A G A T T T A A T A C T T A G C C A T C T A A C A C T T C A A G C A T A A C
WI-6194	105	T A G A A A	C A C A T G G C A A T G A T A A T A A A	T C T A T C C T C A G A G T G T A G T C T G C A	A A G T G A T G T C C T C A C A A A T A C A T T T C T C A A C T C A A A C A C A T C A T G C T T G A A A T A T C A C T G A A C T T G T C A C C A A G A A G T C A C A T G G C A A T G A T A A T A A A G A A A T T A J A T G C A G A C T A C A C T C T G A G G A T A G A G C T C T A A G A G A T A A A C A A T G G A A T T T G G A A A A A T A G G A G T A A A
WI-6213	164	C T ---	---	---	C A T A T G C T G C T T A T T C T G T A A G G A T A C A C T G A A A C G T T A G A T G A T A A T A G C T A A T A G C A A G A A T G T A G A A T G A G G C A T C A G C T T C T A A C C A C T C T C A A G A A T G T T A G T A T G T A T T G T C A T T A C A T G T T T A C T T T G A T A T T G T C T C A T T A C T A T G T C T A T A T A T A A T A T G T A G A T A C A G T A A G T A A G T A G T G A T C C T G C A T T T C A G G T A A G C G T A G G T G G A A T C C A G A T T T C C T C T T G A G G A A A
WI-6217	131	C T ---	---	---	C G G G T T A A G A A T A C C T T T A A A T T A G G T A A T A A A G C T C A A G G A G G T G G G C T G T C A T C T G T G T G T C A G T C C T C T G C C C C T G G C T G T C A G T G T G C T C C A G G C C T T G A C A A G C A G C T C A T T C A A G C T G G C C A C C A T G G C C T A G G T C G T C A A C A A G T C C A G C A G C A A T C A T G G C G T T C T C G T A T A T C T G A T C C
WI-6238	175	G A ---	---	---	A C A T A G T C T T A T T T G T C A A G A A G G C T A C A C G G A T C A C T T C T G G T T T T G T T T T A T G C T T T T T T T T T T C T A G A A G G T A T C T A C A T C T G C A T T A T T T A C A G C C T T G T G T A T T A C A G A T C A A G A T A C A G T G T T A G A A C A C A A A A G T T G A G A A A A A A A C T T C T C A A A T T G A J G T T C C A G A C T T C A G G A A A A T G A T T T C C A C A T G G T A A G G C C A G A G T C T C A G T G T T G T C A T C C A G A A G C A G C T T G
WI-6272	86	C T T A A	G C A T T T A T T C A G G G A A A C T T	C T G T T T T T G G A G A A G A C A A A G A A	C T T G A T T A A T C A G G C T T T G G G T C A T A G G G G A T T A G T C A C T G T C A G A T C A T A A T A A T G C A T T T A T T C A G G G A A A C T T T A A T C T T T C T C T C C A A A A C A G C T G C T G G A A C A C C T C A A A T T A A G G G A T G T C A T C T A A A A C A C C T T T A C T G A A C T T G A T T C C T T G G C C A G A G A A G G T C T T A C T G T A G C A G A G G A C T T A A T G C A A T G C C T A T T C G G G C A A T A A A T G A A T A C T T G A T G C A T T C A T A C A G G C A A G A A T C C C A G C A T C C C A G A A G C T C T G T C G C G A J C T G C A A A G C C A T G G C T G C A G A C A T C A G G A A G C T G G T C A G T T C T A G T C T G C C T C T C G A T T T C C C T G C C A G C A G T C T C T C T C A T T C T C T G G C C
WI-6303	98	G A C T C T G T C G C	C C C A G A G A A G	C A G C C A T G G C T T T G C A G	T C T G A T G C T T T T G C A T G A T T C T A A T T A T T G C C T T T T C A G A G C T C T G C T G T G T A A A A A G T G G G T G C C A T A C A A A C A G T C C C T T T T C A A G C C A G C G T G C A T C C T G C C A A T C A A T C A C T G T A A T G T C C A T T G T C C A A A C A G G T C A A C C G T T G T C C C A T G A A A A C T G G A T A A A G A G T T G C T G A T A G T A G T G T C T G T T C T C C C T T T A C A T C T T T T G G G G A
WI-6315b	193	C T ---	---	---	A T G C T T T T G C A T G A T T C T A A T T A T T G C C T T T T C A G A G C T C T G C T G T G T A A A A A G T G G G T G C C A T A C A A A C A G T C C C T T T T C A A G C C A G C G T G C A T C C T G C C A A T C A A T C A C T G T A A T G T C C A T T G T C C A A A C A G G T C A A C C G T T G T C C C A T G A A A A C T G G A T A A A G A G T T G C T G A T A G T A G T G T C T G T T C T C C C T T T A C A T C T T T T G G G G A
WI-6315	187	T C ---	---	---	A T G C T T T T G C A T G A T T C T A A T T A T T G C C T T T T C A G A G C T C T G C T G T G T A A A A A G T G G G T G C C A T A C A A A C A G T C C C T T T T C A A G C C A G C G T G C A T C C T G C C A A T C A A T C A C T G T A A T G T C C A T T G T C C A A A C A G G T C A A C C G T T G T C C C A T G A A A A C T G G A T A A A G A G T T G C T G A T A G T A G T C T G A T T C T G T T C T C C C T T T A C A T C T T T T G G G G A

WI-6375	28 A G A A	GGTTATTGCA TATGGAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTATTGCATATGGAAATCAATAGAGTATCTTTACAAAAAAGGTTAGAATAAAGATCTC ACATTTGTAAGGCACATATGAACATTTTATAGCAAGCACAAAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGATGAATTCATACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAAITTAJGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGCTCAACAGATGAATTCATACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACATATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGATTTCGAGCAGATTTCATTATAGTTACTTAA CAGCTAAATAAAGGGTGATTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[GT]TATCAACCTTCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 G T C T G	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGAAACAGAGATGGGC TCTGTAGTCCAAACAGGATGTGGACGTCCTGTAGTCTCTCTTTTACACAACCTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCAACAACACGACGTAACCTCTGAGAGAAAAC[CG]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATTAATAATTACATGGGCTATTATTAAGGACATTGTGTATGTTTCCACTTTGTTTAAA [CT]TAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAGTTTGAAAAATGGCG
WI-6558b	68 C T ---		---	ATTGTAATTAATAATTACATGGGCTATTATTAAGGACATT[GC]GTAAATGTTTCCACTTTGTTT AAACAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAGTTTGAAAAATGGCG
WI-6558a	42 G C ---		---	AACCAACAAAACCTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAA AGTTGTCATAT[CG]AGCAATGGATGCTGTGTCAGAACATAGTCCCAATAAATTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGATGTAAAGATTATGGAAGAT ATCGTGAGCCAAAAC
WI-6629	75 T C G C A T A	TCTTTTCAGAG AATAAAAAGTT	TGACACAGCAT OCATTGCT	CTGCCCTGAACCAATCAGATTAGTTTAAATCAATCAATCAAACTCCAGCTGTTTCTCTGCTTT TTACTTAGCAAGGAAACCTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAATTTCTCAAGCACA T[CG]ACCCAACTTGAAGGTGATTGAACCCCAAAATAATGGGTGGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAAGCTATCTGGTTATATTTTGATGTTGCCAAT
WI-6644	134 T C ---		---	TGCTAACACACCACCATTAATTAAGGAGAGTACTAGGAAAACTACCAACACAGCATGTGAACACAGT TGGGACGGTGGTAAAGGGCACAGACTCTGGAGCCACAGC[CT]GGCTAATACACTGCAATATTTTA TGTTAGCAATTAATAGCTGGTCTGTGTATAACCAGAGAGCGGTATCTGG
WI-6680b	106 C T A G C C A C A G C	CAGACTCTGG	ACATAAAATA TTGCAGTGTAT TAGCC	

WI-6690a	28 T C	AAACACCACC ATTATTAAGG AGAG	GCTGTGTTGG TAGTTTTCTCT	TGCTAAACACCACCATTATTAGGAGAGT/CJACTAGGAAAAAAGTACCAACACAGCATGTGAAAC AGTTGGGCACGGTGTAAAGGGCACAGACTCTGGAGCCACAGCGGCTAATACACTGCAATATTTTA TGTTAGCAAATTATAGCTGTGTGTATTAACAGAGAGCGGTATCTGG
WI-6770	53 A G	CAACCCCAA AACATCACA	GTATAATAGTA TGAATAA	GATGTTTAATGACACAGATCTTCCAAAGTAATCCAAACCCCAAAACATCACA/JGJAATTATTATCAT ACTATTATACACTCCAAAAGCAAATACTTCAACTGCAATCC
WI-6686	151 A G A	GCATTCTCCA AAACAAAAGA	CCTTGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTCCAGCAATCAGCTAGCACTAATCTTGACCAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTTAGATGAAATTTACATTTAAACATGTTAACTCCAAGCATTCT TCCAAAACAAAGAAT/JGJAACATTGGAATAGTCACCTTACAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGAGATCTAACAGCTGCAGAAATGG/CJACTTCTCTCCAGCTTTTGTGAACAAAAC AATCTCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGTTGTTTCAGGTACAAAGTCTC
WI-6844	225 T C ---		---	TAAATCTGCCAACTAGCATTACGTCCACTCTTGCCATCTTAAACAAAGGGTATTCTCTCTTG GTATTTCAAATGATGCATTATACAATAAACGAAGTTAGAACTTAAATGCACCTGATTAAATTATG TAACTGGTAATTTGTTTTAAAGCATAATAATTTGGTCTCTTCTTCAATAAATGGAAATTTAAA TATTTCTCTGATAGTCTTGAGGTT/CJATCATTTATGATGAGTAGTGCAAAAGTGTG
WI-6824	112 A G ---		---	CGGTTTGTCTACACTTAAATGGGTTTTTTTTAAGGGATTTTTTTCAGGTCTGTGACGAACATCAA ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTCTGCCAA/JG/CACCTTAGAAAAATTTACAT GACACGGAGAAAAATGCGCCTCTTGCTCTTGAAGAGCTTACAGCTTAGGGATTGACAACTCACAGT CTTAGGAAGTGGCAAGTAAGGCAAAATCTTCTATCCCTAGAGCTATTGTG
WI-6889	139 T C AATC	GAAAAATGAG ATGCAGTTAA	TCACTTTGTGG CTTTTAATTAT TCT	GTACAAAAAGCTGAGAGAGCCCAACATGGAAGTGTCAAGAAAAACATTTCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAGAGGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC/CJAGAAATAATTAAAGCCCAAGTGAAAGTGTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C ---		---	TCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACCTCAAAATATCTGATGAACCTTGATGAACGTAA AAGAGGTCTCCTTAAACAAGATATCATCTCCGAAAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAAAGTTTGCCTTCCCAAGGAATGTGTTCTAATTTGGTTTCAAAAGCACACTGGTTCC CACCTTTACCACTT/CJCATGACATTGGACAATAGTACTACTCTTTCTAC
WI-9413	112 G C ---		---	GCCAGTCTCTAGTAAGTCTTAGGGACATGACCAAGCAAGAGCCCTGTCTTATATGAAGACAAAC AGGTGCCATACCTGGGTGGAGGATACCGCTGCTATCCAGATG/CJAGATTTGGTGGAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAAACAGAGGTATGA
WI-9557	74 C T ---		---	AAAAGCTTTAAAAAAAAGTGGTGTCTATCTTTAGAAACACTTTCAGCAAGATCAAGTAGCCCCAGCT ACAGCCTC/TGGTGCATCTTAACCCCTCTCCTTTT

WI-9617	37 G T ---				TGCTCTTTTATTTACAGTTTCACAACACACGCGGTG[G/T]TGGCACAGTCTACCAAGTGCCCGCAG CGCCACGCTTGGCCGGAAGTCTCATCTGTTGCTCTATGACTGATGAATTTGGGATGGCCAG CTCCAGAATGTTCCACGTTGGGGCACTCTGTGGCAGAGAGGCTGAGCCCTTGCCACACTGGCAACCA AAGAGTTGCACGATGCAGCTGCAGTGGTCCAGCCGGTGTGCTGTG
WI-9657	121 T G ---				AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAAGT/GJATAATTCTT TGATTAATAATAATGTTTATAAATGTTTATGAAGTCAATTACATTATCTTTTAAATAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAATTAATGCTTTTGATATAGATTGAGG
WI-13119b	114 G C GCTGGGA	CC'TCCCAAGTA	AAAAATTAAAC	CAGGTGTGGTG T	CAGGGTCTGCTGCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT OCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTG/CJACACCAACACTGGTTAA TTTTTTAATTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAAACAAACCACTAAC CAGGGTCTGCTGCTGCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTC/GJACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACTGGTTA ATTTTTTAATTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAAACAAACCACTAA C
WI-13119a	51 C G ---				ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[C/T]CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAGAAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACACTATGGCAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-13112	71 C T AGCTTTT	TCATAAAGAC TACAGACTTA	GGAAAAAG		TGTTAACATTTTATTGGTACGTGCTCTCAGTACAAC/CJAAACAGCATCAGTAGTGTACACTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAGAAAGCCCAAGGTGAGAAGTATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCATCTTTATCTTCCCTGTGGATGAGATGTGCACACACAAGT AAA
WI-12988	36 C A CTCAGTACAA	GTTT			TGCTATTTCATGACAGACACGTGAGACAAAATATCTTATTTACAGATGGAAATAGACCCAGACATTA TTCAGTACTTTAACCACATAATAGTGGAAACCCCTGAGACTTTAG/JATCTGCAAGGGGTTTAAATAAT GCAAAATATCACATATATTTCCATTTTAAACACCATATTTAAGTTTCCATTTCTTAATAGAAAAATGA TAAAAAATGTTTCCCAATAT
WI-13020a	108 G A CTTT	CTAATAGTGG AACCCCTGAGA	CATTATTAAAC CCCTTTCAGA		TGTATAAAAAATCCAACTGTTCCACAAGTACATATGCTCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCAA/GJTACAAAAAACAGCATTTCCCTATGGCCAGTGTCTACAGAAAGT AAGACTGTGCAAACTTTTATCGTATAGTCAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAAGCA AGTGTGTGTTT
WI-12837	87 A G AAAGTCCA	CCATATACAT ATATCAAGGT	GCCATAGGAA ATGCTGTTTT		AGTGTGTGTTT

L42611b	50 G C ---			GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGTCCTCTCAGGTTGCGCTGTGTCG/CJTCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCAGCTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTTATTCACCA CTGGAGCTTCACTTTGTAC
L42611	34 T C ---			GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGTCCTCTCAGGTTGCGCTGTCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCAGCTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTTATTCACCA CTGGAGCTTCACTTTGTAC
WI-1172b	179 C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG	TGAACGTGTGGTTAAACATAGGCAATTGGTTAAAAATCAATTTAAAAAACAGGCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCAGCTCAGATTATGTTCTTGAATACCATTTTCTGCTTTC AAAAGAAAGACATGAGGCTTCTTGAAGAAATGGCTGATACCAAG[CJTCTGCAGTGAAAAATGCA CATGATGAGCTGGAACATGTTGT
WI-1172a	17 C A ---			TGAACGTGTGGTTAAAA[CJTAGGCAATTGGTTAAAAATCAATTTAAAAAACAGGCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCAGCTCAGATTATGTTCTTGAATACCATTTTCTGCT TTCAAAGAAAGACATGAGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAAAATGCA CATGATGAGCTGGAACATGTTGT
WI-1177	35 G C A	GCAGATTGGA AGTGTGAAAA	CACCTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[CJAAAGAAAAAGAGTCTAAATATTTCAG AAATGTAAGTGTGCTGCCCTCAACTGTCTTTTACCCACTTAATCTGCAATTTTGAAGAACTAGATTGAAT TCCTTTGCAAAACCCCTTGCCATCATGGATACCCGAGTTAAACCGTTAATTAAGACATTAACACATGG CCTGGTG
WI-1231b	141 G A ---			TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCGCCATATTC CAACTAAGCAGGAGTGTTCACAATAACAACATAGGCTCTTTATCTCCTCTTTTCATTAATTTCTT TCAC[CJATTTATCCCTCACCCCTGAACGCCCTTCTCCTCGTAGTGACATTTTAAAAATCCACTTTAC ACATTGGACC
WI-1231a	126 T C A	GGCTCTTTATT CTCCTCTCTTC	CGTTCAGGGTG AGGGAATAA	TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCGCCATATTC CAACTAAGCAGGAGTGTTCACAATAACAACATAGGCTCTTTATCTCCTCTTTTCATTAATTTCTT CTTTCACGTTATCCCTCACCCCTGAACGCCCTTCTCCTCGTAGTGACATTTTAAAAATCCACTTTACA CATCGGACC
WI-472	114 G C ACAGAAAAAG	ACATACATAT CCATTATACA	GACCTTTCTTT TCCAGCCC	GAAGGCAGGACTGTGTTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTATTTTAAATTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAAG[CJGGCTGGAAAAAG GTCAAGTGAGATTCAGATATTTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

[illegible]

WI-5791a	44 C G ---			CTATGATTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCGACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTCTTATTTTGGCCACCCTGTTTGT TAGGAA
WI-5406c	120 C T ---			CACCTGCTGTTGTTCATGGGTGCCACAGACTCTTCCAGAAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCTCTTTATGAGCCAC ACTTCTCATTTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGAAAGAGAGAGGCAA GG
WI-5406b	118 C A A	OCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT	CACCTGCTGTTGTTCATGGGTGCCACAGACTCTTCCAGAAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCTCTATGAGCCAC ACTTCTCATTTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGAAAGAGAGAGGCAA GG
WI-5406a	42 A G ---		---	CACCTGCTGTTGTTCATGGGTGCCACAGACTCTTCCAGAAAGAGCCACTTCCACAGATGCAACAG GCCTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCTCTATGAGCCAC ACTTCTCATTTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGAAAGAGAGAGGCAA GG
WI-5798	48 G C TG	TTATTCTCC TTGTTTCTTT	ACTGTTAGAAA ACCAAGTATTT TCAAT	CCATTCCTCTCTCCCTCTCCCTTATTCTCCCTGTTTCTTTTGCGATTTGAAAAATCTGGTT TTCTAACAGTGTGCTGTGATGGATACTATGTTATACATGCATAGTTCTATATGGGTATCA
WI-5415	54 T A TTT	TCTTCATGAAT TCATCTTTCAG	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTAAGCACGATTGTCTTCATGAATTCATCTTTCAGTTT/AJTAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41 C T G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACTCCAGAGAAAATCCAAGAGCTCTTAAACCATAATTTTGTTTA GAACTCCTGTGCCAACCCACTCTTGTGATGTGAGTGAC
WI-5481b	131 A G CTG	TGTCATTTATG CTGCAGTCG	TTACTTCCAGG CTCCAAGTATT	AAGCCAAATTCACATTAGTTGATGAATTTG/AJAATTTTACAGTATCTAATGCATGGGCATCTGTTCAAC TCTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTGTCAATTTATGCTGCAGTCG/A/GA ATACTTGGAGCCTGGAAGTAAGACTTGGCTATTTTCCAAATTA
WI-5481a	29 G A AATT	CCAAATTCAC ATTAGTTGATG	CCCATGCAATTA GATACTGTAAA ATT	AAGCCAAATTCACATTAGTTGATGAATTTG/AJAATTTTACAGTATCTAATGCATGGGCATCTGTTTC AATCTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTGTCAATTTATGCTGCAGTCGAA ATACTTGGAGCCTGGAAGTAAGACTTGGCTATTTTCCAAATTA
WI-5492	38 T C ---		---	TCATGAGTCTTCTTCAAAGATGCTGTTAAAGTCCCATTC/CAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134 T C	---	---	TATTTTTTTTCTCAATCCTGGAGCACACCATGCTCTTTCTATTCTATCTTCATGCTTCACATTTATTTTTT TTTACATTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATCTTTAGT/C/
WI-5546	40 C T A	CCCAATACTTT TTCAGGTGAA	CCTGTATTTTA GCAACATGGG	TTTCAAATTAAATGCCACCATAGAAATAATTTCTAACCAACCAGCCAAACAGCCTCACTCTTCCTT CCTGGTGCAATTACTCTTTACAC
WI-5552	97 C T	GGCAACAGCCT TTTTAGAGT	TGCACAAATTG CCAGG	CCTTATAACCCCAATACCTTTTCAGGTGAAAAAGGGGAAA/C/TTACCCCATGTTTGCCTAAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGAATTCGTGATGTGGGAAATAT TAGAAAATTAAAGCAGAGAGGCA
WI-5836b	161 C T	---	---	TGTTTGTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTTGATTGACGGGTATGGGT GGGGCTATCGGCACCAGCCTTTTAGAGT/C/TTCTGGGCAATTTGTGCACTAGTGTCAAG TAAGTTGATTTAAACACTCTGTGCCTCAATTTTCTCACCTATAAATAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAAGTGGATAGACATGAATACTCTGATGATCTGTTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT/C/TTCCATTTTGAAAAATTAAAGCTTTTGAATTGTTTTTCCA ATG
WI-5573	58 C T	GTTCAATAGG AGGTGGGA	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATCGGTTACCCCTCGATGATGATGGGGTTCAATAAGGAGGTGGGA/C/TTGACAC ATTACTCTCCAACCTGTTTCATCAGAACACTTCAACAGCG
WI-5850b	134 G A	---	---	CAGGACCTGGAGCCTTTGCTGTTTGCTCTTCCACCCCTCACTCTTTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTCTATGCA/C/TTGGGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTC/G/A TTTTGCCATTTCTGTATATCAACAGAGAGAGGGTGG
WI-5850a	92 C T	---	---	CAGGACCTGGAGCCTTTGCTGTTTGCTCTTCCACCCCTCACTCTTTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTCTATGCA/C/TTGGGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGGGTGG
WI-5612b	125 A T	CTATTAATGA GCATCGTGCA TTC	TTCTCTTGAGA AACCTAAAAAC ACTG	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATCTTAACATCAACAATAATCTTATTTCTGCCTG TCACACTAAATTTGCAAGCATTCAATTGATTGACTATTATGAGCATCGTGTCAATTCATTCAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTTCTTCTGTAACCTCAAGTA
WI-5612a	44 T A	---	---	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATCTTAACATCAACAATAATCTTATTTCTGCTG CTGTACACTAAATTTGCAAGCATTCAATTGATTGACTATTATGAGCATCGTGTCAATTCACAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTTCTTCTGTAACCTCAAGTA
WI-5636	26 A C	GCCAAATTTAT CCGCAATAA	CATCGAGGACT TTGGGA	TGAGAGCCAAATTTATCCGCAATAA/C/TTCCCAAGTCTCGATGGAGGCATTTTCAGAAATCGGG GCAGGGAGGCAGAGGTGAGACAGATGTGAAGAAC

WI-5865c	103	C	---	---	CTAGTAAGTT TCAGTCATTG ATATGT	CTCAGACATTCATTTTCATTAGTTGTTAAATTTTGTGTAATTCATAGCATGGATAATATTATACAGAA AAAAATTT/GTACATATCAAAATGACTGAAACCTACTAGGTAGCAATTTGTTTGTCAATTTGCT CATGGAGCCGACGTTACGCTCTCAGTTTTTCCATC/TJTTTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTTCGTATTTCAACTCTCATCTGCTGATTGGATGGTAGTCATAAAATATGGGTGATTC AGAAAATAAGTAAATG
WI-5865b	99	T	A	---	---	TTAGAAACCTCCATTTTATTCTGCCATGGTACATCTTTTAAAGAACTTTTTTAAAGAACTTTTTCATTTATGCATTC ACTGACTCACTCACTTGTCTATCAAAAATTT/AJAAACAAATATTAAATATTTTATTTACAGAGGAA CTCAGAACCCAGAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAGACAGACAACTAAATAAATCCAGG
WI-5865	165	T	A	---	---	TTAGAAACCTCCATTTTATTCTGCCATGGTACATCTTTTAAAGAACTTTTTTAAAGAACTTTTTCATTTATGCATTC ACTGACTCACTCACTTGTCTATCAAAAATTTAAACAAATATTAAATATTTTATTTACAGAGGAACTC AGAACCCAGAAAATGACCAAGACACAGT/AJCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTC AGAGAAGACAGACAACTAAATAAATCCAGG
WI-5874	76	T	G	ACAGAAAA	CATAGCATGG ATAATATTAT ACAGAAAA	CTCAGACATTCATTTTCATTAGTTGTTAAATTTTGTGTAATTCATAGCATGGATAATATTATACAGAA AAAAATTT/GTACATATCAAAATGACTGAAACCTACTAGGTAGCAATTTGTTTGTCAATTTGCT
WI-5752	36	A	T	TTTTTCCATC	CAGCCTCTCAG AGAGTAAAT ATGAAAAA	CATGGAGCCGACGTTACGCTCTCAGTTTTTCCATC/TJTTTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTTCGTATTTCAACTCTCATCTGCTGATTGGATGGTAGTCATAAAATATGGGTGATTC AGAAAATAAGTAAATG
WI-5760b	61	C	---	---	---	TTAGCAGAAACAACAANAATGTCACAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAATA/C/G/C CATTAGGTATTAGATAAGCATCCCATAAAACATTGTTGAAAACGAAGCCGAGTTTTCGATTTCACACA GTTGCTGTTTTAACCTCTCTAATCCCGATAATAGCCATTAGGTATTAGATAAGC/G/A/JTCCCACGAA CATGTTGAAAACGAAGCCACGTTTTCCGATTTCACACAGTTAGTTGCTGTT
WI-5760	187	G	A	---	---	TTAGCAGAAACAACAANAATGTCACAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAATAACCCAT TAGGTATTAGATAAGCATCCCATAAAACATTGTTGAAAACGAAGCCGAGTTTTCGATTTCACACAGTT GTCGTTTTAACCTCTCTAATCCCGATAAATAGCCATTAGGTATTAGATAAGC/G/A/JTCCCACGAA ACATTGTTGAAAACGAAGCCACGTTTTCCGATTTCACACAGTTAGTTGCTGTT
WI-5944	52	A	G	GGAATCTTG	TTCTCACCATG AATCTGATCTG AATCTGATCTG	AATATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTG/A/JTGCAGATTAGAT CCCACCTCACTATTGAGAAGCTAAAGTGAAGACTACTCATTTCTCAGTCTTCTGCTG
WI-5967b	148	C	T	---	---	GAGTTTAATGAATCCTGTTCCCTCTAAAACCTCCTGTTCCCTCCCACTTCACATTTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAAATGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTA/C/JTGTGCTGTGCGGTATCTGCTCCCAATCACCCATTCCACTTTATTTCTCTATTAT GCTGAATGAACGGTTATATTACAG

WI-5967	165 C T ---				GAGTTAATGAATCCTGTTCCCTCCTAAAAACCTCCTGTTCCGCCAACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGCTCTGTGCCGTATC/TGTCTCCAATCACCCATTCCACATTTATTTCTCTATTAT GCTGAATGAACGGTTATATTACAG
WI-6093	53 G C ---				GGGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA/GC/GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTTCAGCTGTCAGCTGAGCCATTGTAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTTCAGCAAACTTTGATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80 T C AGGTACTT	CTTCTTAATTA AGCATCTACA			GACTCTGTCTCAAGAAAAAATAATGAAAAATTGAATAATTATTAAAGCACCTTCTTAATTAAAGCAT CTACAAGGTACTTAT/CJCACTGTTCTGGGGTTTTCAATCTCTTCACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAAAACAGGATTGTTACATGCAGAGAAATAGGGGGAGATAAAAAATTTGTCTTTT CTC
WI-6450	45 T G TGTCACA				ATAGGACAGTTTTTCTTCCAAATGACTTATTCTATATCTTGTCACAT/GIAGAAGTACCACACATTTC AACAGAGCCAGGCTATGCCAGGGTGGGATTATTTACAGTCATGTAATATGCATGTAAAGACTA TTTTACTGGCCTCTTTATGCATAAAACAAGGTATTGGTCTATTCAACAACATGTGTCAATACAG CAGTTGTCATGTCCTCTGCTACTAGAATATAGTCTTTATAGAATATGTGGTTTAGAATAAAGCCACA AATTATTCTATAAAACAACA/CJTAAGGAACGAGGCTCAAAAGTGGAACAAAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAAAATATAATCCGTGACCTCTTA
WI-6461	88 C T ---				GAACTATCCTTTAGTGGTGCCACATTTCTATTCTGATCTTTGGTCACACAGGACCTTTCTGGGCT ATGAAATAGTCTATTTCAGTGAAGTATGATCAATAAAGACATGCAAAAACCTTTTCACAGTCTTTGT CCTGG/GJAATATCTCACAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCTTT
WI-7466c	141 G A TTTGTCCTGG				GAACTATCCTTTAGTGGTGCCACATTTCTATTCTGATCTTTGGTCACACAGGACCTTTCTGGGCT ATGAAATAGTCT/CJATTTCAGTGAAGTATGATCAATAAAGACATGCAAAAACCTTTTCACAGTCTT TGCTCTGGGAATATCTCACAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCTTT
WI-7466b	80 T C GTC				TGCTTTTAAAAATAACAATGACCACCACCTGACACCATAGTCTGTCTCCATTTGCCACGCTTCTCCTC AGTAGAATAAGACAGGACTTTGCTGGTGTCTATCT/CJATTCTCTTCAGAGAGACACTTTGGCCCT CATAGGCATTCATAGATATTTGTTGAATGAATGTGCTTTTGCATATTGATTCCTACATTTGATACA TTCTCAGGAGGACATTTGGCCTAT
WI-9814	104 C A ---				CCTCTAACAGAAAACTTGACTTCTCCTCAACTCAAAATACCCCTTCTCTAATAATTTT/GJAGTAACCA AAATATCTCTCAAAATAAATTATCTTTAATTAGAAAGCAACAGTGTAGAGGTAGTACATTCA CCACC
WI-9720b	55 A G ---				

WI-9720a	47 A G ---				CCCTAACAAAGAAACCTTGACTTCCTCAACTCAAAATACCCTTCTCTGATGATATTTAAGTAACCA AAATATTCCTTCAAATAAATAATCTTTTAATTAGAAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---				CACGCTCTAAGGCAGGATGTGGCTTATGAGATACTTTGCATTGTCTGTCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTGCATGTGCAGATGAAGGCTCAGGGTCTTATGAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTAGTTGCATT TAAGAAATGCCAGTCTTTTGCTGCATCATCTTGAACATTAATCCACATG
WI-9748	74 C G ---				CCACTTCAGTAAATCAATTTGTAGCACTTATTTCTAAAGATTTCTAATTTTTATATGTTTACCCTTT GTCATTTCGJTCAGACCAAGTACATGTTTTACACAGCCATCTTTCTCTGGAATCTTTCAGAAT TACAGTTATGATGTCTTTTATATTCCCA
WI-9943	91 T C ---				TGAGGCTATGATTCAGATTGTAGTACTAATACTTATTAAGCAATTTCAATGTTGTGGCACTGTT CGTTGTGTTTTATATCCATCTTC/CJATTTTAAATTTCTACTGAGCAGAAAAAATAATGTATACATT AACCTTTGCTCCCTATTGTACCTTTTAAATATTGCATTTCACACCTTCCTTTTGTCAATTAGGGA
WI-9891	39 T C ---				AGGGCCCTTCACAGATCCGTCAGCTCAACACTGCCTCTTCJAGTGAGCCTGTGAACACACCCAAAGAC GGCTGGTCATCAGTGTCTCTCTCTTTCCGGACAACATCTTTAAAGAAAAAAGAGAGTGT CTTTGAATGTATCCATTTATCCCCAAATAATCTTGTTTAAATAATCTCTATTAGGCCAAATCCAAT GTGCTGAAATATCTGCCAAGCATGTCTTACACAAAAGGATTGCAAA
WI-9897b	84 C T ---				CTCAGAAATTTATCAGATCTCCCCAAATGTATGATCTTGTTCTCAACATCTATTTTCTCTCAAAC ATTTATCTAGCCTGTATC/JAAGTCAATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83 A T ---				CTCAGAAATTTATCAGATCTCCCCAAATGTATGATCTTGTTCTCAACATCTATTTTCTCTCAAAC ATTTATCTAGCCTGTATC/JAAGTCAATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115 C A ---				AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTTCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGAGCTGGCAGGGGGAGTTCAGACA/CJ/JAGCCAAAGAAAAGCC TGATATTAAAGAGGCACITGCATTAA
WI-9935a	42 C T ---				AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTTCACACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGAGCTGGCAGGGGGAGTTCAGACACAGCCAAAGAAAAGCC TGATATTAAAGAGGCACITGCATTAA
WI-9983	146 C T ---				CCTGTTAGGTGCCAGAGTCCATGCTCTGGCCACAATGTTAGGCTGCCTCCCATTTCTCTTGTCTTGA TTCCCCAAACCCAAAGTTCTCACCCTCAATCTGATCAATGCTGACTAGGTCTAGGCTGCTCAGGGTAA AGCATTATGA/C/JAGACACAAAGACAAAGAGGTAAAGTTGCTGTCTCTCAAGAGAGAGACATAA AACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T A T C T	T G A T G T A A T G C T A T G T A G C A A	T T G A T T A C T G T G C T T A G G G G A	A T A T C A G T G G T T G A G T A T A C A G C A A T C T A T T T T T A T T A T G T G T G C T A T A A A T C A A T C A A T G G T T C T A C A T T C A A A T A A G A T C T T T T G C T C T C T G C T C A G A T G C T T T C A A T G A T G A T A T G C T A T G T A G C A A A T C T A / A T T C C C C T A A G C A C A G T A A T C A A G G C C T T C T A C C C C A
WI-10020b	122	T A T T T	G C G A G A A A A G A A A T C A T G A C	G A C T G T T A A T T T A T T T A A T C A T T A G T C T G G	T T A C T T C A T T G T C A T C T T G A C T G C T A T A A A T A A A T T A T G T T A A C T G G C T C T G A A A G A A T T T A G G C A T G C A T A G A A A T A G C A G T G T T T T A T T G C G A G A A A A G A A A T C A T G A C T T T T T / A A A A A T A C C A G A C T A A T G A T T A A T A A A T T A A C A G T C C T A G G G T T C C G G A A G T G C C T A A A G C A C G T A G T A G C C C T C C T T A G A
WI-10020a	39	T C A T A A A T T	T G T C A T C T T G A C T C G T A T T A A	A A A T T C T T T T C A G A G C C A G T T A A C	T T A C T T C A T T G T C A T C T T G A C T G T A T A A A T A A A T T A / C / G T T A A C T G G C T C T G A A A G A A T T T A G G C A T G C A T A G A G A A T A G C A G T G T T T T A T T G G C G A G A A A A G A A A T C A T G A C T T T T T A A A A A T A C C A G A C T A A T G A T T A A A T A A A T T A A C A G T C C T A G G G T T C C G G A A G T G C C T A A A G C A C G T A G T A G C C C T C C T T A G A
WI-10084b	170	C T T T A C A T G	C C T T T A G A T A T A T T G T G A T T G T	A C C T T T C T G A A G C C A G A T T T C	T C T G A G T C T T T C T G A G A C A C T T G C C A T G G T C A A G G T A G C A G G A T C A G G A A G G C A T T A T A A T A A A T A A A T T T G C A G A G C A T C T C T C C T A T G C A C C A G A T A T T G T G T G A C A C T C T G T T A T C C A G T A T C C C T A C T C C T T A G A T A T A T T G T G A T T G T T T A C A T G / C / T G A A A T C T G G C T T C A G A A A G G T A G G T G T T T
WI-10084a	54	C A G G G A A G G	G T A G C A G G A T C A G G G A A G G	G A G A T G C T C T G C A A A T T A T A T T T A T T A T	T C T G A G T C T T T C T G A G A C A C T T G C C A T G G T C A A G G T A G C A G G A T C A G G A A G G / C A / A T T A T A A T A A A T A A A T T T G C A G A G C A T C T C T C C T A T G C A C C A G A T A T T G T G T G A C A C T C T G T T A A T C C A G T A T C C C T A C T C C T T T A G A T A T A T T G T G A T T G T T T A C A T G C G A A A T C T G G C T T C A G A A A G G T A G G T G T T T
WI-10289	29	T C C A A C T C T T	T C T C T G T C C C C A A A C T C T T	A T T C T T G T T G T A T T G A A T G G A A T T A A	C C A G G G A T T C T C T G T C C C C A A A C T C T T A T / C / T T A A T T C C A T T C A A T A C A C A A G A A T T T A T A G A A T A T G C A C C A C A T G C C C A C A A A G A C A C C C T T A T A T A G T
WI-1319	40	A T A T T C T T T	T G G C A C T T A G A A C A T A G T T T	G C C A C A C A C C C C T A T G G T	A A G A A A T C C T T G T G G C A C T T A G A A C A T A G T T T A T T C T T T A T T A C C A T A G G G T G T G G C T T A T C T T T T A C C T G G C A T G G C T T A G G T C C T G T T A T A A T T G G T A T C T T T T T G C C A C A A A G A G T C T G T T C T G A C A G T C T T A T G A T C T A T T T A A C A T T A A C A C T G G T C A G A T G T T T A A A A C T T G T T G A A C C T G C A G C
WI-10316	104	T C C T C T T	C T G T T G A T T T C T A C C T C T A T T	G C T T T G G A A T G T A T C C A A A A G T T T	A G C A A C G T G T A C A A C T T A G T G A G G T G T A A A T C A G A A G C A T C T A T A T T A T T C A C C A G T C A C C A C C C T G G A C T A T A G T C T G T T G A T T T C T A C C T A T T C T C T A T / C / T A A A C T T T T G G A T A C A T T C C A A A G C A T C A T G G T C A C T T C C A G T T A T G A A A G G A T G T T A A A A G C C C A G C C A G T G A G T T G T G C A C A A T T T T G G A G A C A T T C T G T A C C C C A C T T A A A A C A C T T C C C C A C A / C / T A C A A A G T T A A C A C T T C A G T T A C C A G G T A T T A G C A G A
WI-2572	61	C T	---	---	---

WI-10368	31 C T	TGAAGCAACC AGGCTCTGTT	CAAGATATTAT ATTATTCTCT AAGAGGGG	GAGGAACCTGCCTGAAGCAACCAGGCTTGTTCCTACCCCTCTTAGAGAAATAAATAATATCTT GAGATAGGAGGAGCAGCTGAGGACAGTCTGGGTTTGTCTACCCCACTGGAAGCAGAAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCCTGATGGATTGCCTTCAGGG T
WI-10391	32 A G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CCTCCGTTCTCTGTCTCAGGTATGACTCCCAAGTCAACTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTTCCAGGGGACGCTGACACAGCCTTTTGTCTGTGTGACAAACAGAACATTCGAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A C	GTTAACCAGA GTCTTCTAATA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT TTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAGTCTT CTAATAGCAAACGAGCTACTGTGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A C	AGCGATGAAATTTATATGTTATGCTGACTTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT TTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAG CTAATAGCAAACGAGCTACTGTGAAGCGGCAAGAAATTTAACCCCT
WI-10567a	60 T C	GGGTGCTCAAT AAATATTATT CTTTT	AAATCTGTT GGTGAAAATTC TAG	AGCGATGAAATTTATATGTTATGCTGACTTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT ATTTTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAGT CTTCTAATAGCAAACGAGCTACTGTGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C G	TACTTTA C	...	CGTTGGGAATATTTCTATCTCACCTAAATTAATGCGGTGATTAATAATATACATTTTAAACAACTTCAAA TTGCTTTAAGTACTTTA[C/G]GAAGACCTTGACTGTGGATTTTGAGTTTTTCTTTTCTTTAATA AAACATGCATATTTAAGTTGTGTCAGCAAGATGCTATATATGTTAATTATCTGATATCAGCATCCCTT TATGTAAT
WI-11153a	33 C A	AATTATG C	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATATTTCTATCTCACCTAAATTAATGCGGTGATTAATAATATACATTTTAAACAACTTCA AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGAGTTTTTCTTTTCTTTAATA AAACATGCATATTTAAGTTGTGTCAGCAAGATGCTATATATGTTAATTATCTGATATCAGCATCCCTT TATGTAAT
WI-2616	125 T C	ATCC	CCATGGCTGTA GTCCAGT	GTTGTAAACTCCAGTATCATTTCCCTCAACCCAGCTTAAATCACAATCAGCTTTTCTTCTCGTA GAGCTCAAACTCAGTCTGAATGAAATTTGTCACAAATGTAAACAGAATTGATCCTATTCAGTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C T	CAAGTGAAAT ATGACCAAAA TGAGA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAACACACACAAAAAGTTTACCACAGTGAATATGACCAAAATGAGA[C/T]AAAT TTGTTAAAAAAAACCTCAAATGAAGAGACAAATATAGTTCAAAGATTCAGGTTCAATATTGT ACCTACAAAATAGGGATAGTCATGGTGTGGCAGACTTTCTTTTCTTTTCTTTTGTGTCCTTA GAATCCATTTTGTCTTTTGGCCAGCATCCCTCTCCCATATTTTAAAGGAGAGAATTCACCTTTTCT CTGTTGGATGATCAGGTTCTGCTCTCCCAATCCAGAGGCGAGTACTATTACCCCATGGGGTCAAT AGAGAGGATTAAACAGGGTGATGCTGCAATGGGAATATTGAAAAACC
WI-10656	59 T G

WI-11169b	154 T G TTTT	TTAACCAAGA GTTTTTCATTC	CTAACTTAAAA ATCCTCATTCGA AAATATAA	CAGCATAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATTTAAGCCTAAGTAGTGCTTTTAAACCAAGAGTTTTTCATCTTTT TTTAAAAAAGAGCAGACATG/GJTATCATGTGTTCTGATAATTTTATATTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95 A G TTGAAAAA	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATTTAAGCCTAAGTAGTGCTTTTAAACCAAGAGTTTTTCATCTT TTTTTTTAAAAAAGAGCAGACATTTATCATGTGTTCTGATAATTTTATATTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25 A G ---		---	CAAGTGCTTGACCTTGATAGGTGAGTGAAGGCTGAAGGTTGGACAGTTGTTGGTTAGTTGGAG ACCAAAATTCAGTCACTCTGTAAATAGATCTTCTCTTTGGTTTACCACCTAGGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTGTCTAAATATTCCAAATAGCCATGGGTTGGACAAAATAC AAGTTAGTGTCTCTTAACCTTAATGGGCATA
WI-10686	133 C T AAGG	TGCCCTGTGC TCTGCTCAAG	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGCACATAAGGCAAACTACTGAGCCCCATACAGAGTGTTTTATGTTAATATTATGAAA AAAGTCAAGAGAACAGATGATAGTTCTGTAGAACTCTGAAATCTGATGCCCTGTCTCAAGG C/TJTGTTCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAGGG GGTAGGATGATTCTAGAAATGCCACTTTACAGCCACTGAAATATATTGCCCTCCCAATGATCTTCTG CTCAAAGAGT/AJTTTTTTTAAAGTTATCTACTATTATATTCTGCTTTTTCAAAAAGAAATGTGAGA ACAGTACAAAATGTGTTTCAGTATAGCAAAATTAATAATTAAGTAAGAAAAAGAAAGCCAAAT TGGGC
WI-10694	144 A G TATGAGTTTTC	TGCAAAATGCTT TGAATTCATCC	GGCATTTTGTA AAGGAGGAAA	TAGAGAGGCTTTTCAGTTTCAGGGTTGGAGGGTGGTGAGGTGAGATTCACCTTTAGAAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAAAGAACTCAGTTCTAAAGTTTCAAGTCTTTGCAAAATGCTTTA TGAGTTTTC/GJTTCCTCTCTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGAAAGCTTTCT T
WI-10716	23 T C C	AGAAAAACAG	TCTCTTTTCTC TCTTGTGTCA TTC	GTGAATTCATCCAGAAAAACAGCT/GJGAATGACAACAAGAGAGAAAAAGAGATAAAGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCCAGTGCATGGAGCAGTG CAGGCCCACTCTGTCAATTAAGTGTTTTGAACAGACACCTCAGTCACACAAAGTTCTCTGTATGT GCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCCTAGTCTGGCTGCTGGCAGTGCTT TTCCAGCCTGCTGCCATAACTAA
WI-10719	115 T C GCCATTCTAG	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	CAACCAATTCAGATTTAATTTTGGCTCTGCTACTTGCCAGATGAGATTTATTTATGTGGGAGTT TCTGAAGATCCCATGGTAAATAGTATCTCTCTCCCTGCTAGGTTTGAAGAAGTTGAA
WI-10721	40 A G CTTGCCA	TGGCTCTGCTA	GAACTCCGAC ATAAATAAAT CTCA	

WI-11204b	88	T C	---	---	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTCACCTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAAAATTATTCAGAAG GCAACATC
WI-11204a	80	T A	A A C T T	T A C C T T T	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTT/AJCACCTTTTATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAAAATTATTCAGAAG GCAACATC
WI-10732	80	C A	A T T G G T T C A C T	A A G A A C A A T G C A T A A C A G A A C T T T A A	ACATGTATTTCTTTAGTGGTCAGCCTTCTTACCCCAAGAATATCCCTGGTTTATTGCTGTGCTTC ATTGGTTCACCT/CJATTAAGTTCTGTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTCOA CACCACCTCTGTTTAACTGTC
WI-11206	127	A T	A C T C	G A G T G A C A A T C C T A A T G G T T G G	TAGTCTTTCTTTGTACGAGTGTCAATAAGAATTACCACCTCTGTACATTTTGTAAAAAGATAGCACAG AGAGAAGCATTACAGGGCACAGCACAAACATGAGGTGTGTTTCTGTATGTACAACTC/AJTCCAA CCATTAGGATTGTCACTCTCATATATAGACAGAATTCAGTGGTGTGATTTGAATTCACACACATGGA ATAAGTCTA
WI-11215	68	C T	---	---	GAAAAAAAGTTTAAATTGGATTGCTTAGTTTGTCTTAAATTTGACCTACTTTCAGATTTTATTTAGT [C/J]ATTTTCTCTATAATATTTCTTGTAGTGATGATTTTCTATAAAATTAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTATTCGAAGCCCCCATTCACCATGT TTT
WI-11219b	89	G A	A G A G A A A	G G T C C T C T A A T T T T C T A C A C T T T C T	ATGAAAAATGCATTAGAAGAAATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAAAA GAGACAAAAGAGATGAAAAATAGGA[G/A]AGAAAGTGTAGAAAAATTAGAGGACCATCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAAGAGGCAAGAAATGAAGGGAGAAAAATCCAC AAAACATCTC
WI-11219a	18	G A	---	---	ATGAAAAATGCATTAGAA[G/A]AATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAAGAGGCAAGAAATGAAGGGAGAAAAATCCAC AAAACATCTC
WI-11222b	136	G A	G G C T G G	C C T G G T A G C C A A G T T G T G A	AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAAATGCTAAAATTGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCACCGTTGAACATTTGTTAAACATTTACCAGCATACCACCTGGGCTG G[G/A]TCACAACCTGGCTACCAGGAGAACCTGACACAGACTTGTAAATTGCTTTCACAGGCTACTGG AAAGCC

WI-1122a	25	C T A	G C C A C A G T G G A A T C A T T T A C	T T T T A G C A T T T G C T G A T T C G	A G C C A C A G T G G A A T C A T T A C A T A C T A C A G A A T G C T A A A A T G G G C T T T G G A T T T T G T T T T G T T T T C C A T A G A C C C A C C G T T G A A C T A T T G T T A A C A T T A C C A G C A T A C C A C T G C G G C T G G T C A C A A C T T G G C T A C C A G G A G A C C T G A C A C A G A C T T C G T A A T T G C T T C A C A G G C T A C T G G A A A G C C
WI-10775	39	C T	T T T A T G C C A T A T T A A T T C A T T A C A C T C	C T A G A T G T A T T T G C T A A G A A A A T A T G A T G	T T G C A A G T T G T T T A T G C C A T A T T A A T T C A T T A C A C T C T A C A T C A T A T T T C T T A G C A A A T A C A T C T A G A C A C C T G G C A C T C A G T A A G G A T A T T C C T G G C A G A T A A T C A T T G T T A T C A T T A G A C A T T G C A G G A C C A C C A T A T G G A T G A T A A A T G T G T T G T T A T A T G A A G G C A A G C A A T T A T T G C A T G C A T T A T A C G A A G G A A T T A A A T A T C T C C T T A G T T G A A T T T A A G T A A A A A A T A A A G T T A C A T A T A A T A C A A A A G T T G T A A G T A G T A G T A A C A A A T G A A T T A G A A A A T T G T C A G T G T T G C T A G T A C A G G A A T C A A A T T T G G A C T A T G A A C A A C A G A C A T A G T T G C T A A G G A T A T T C C A C A A A T T A T T T C A T G A
WI-11226	165	A C	G C A A G G G A G G A A C A T T T A C A	---	C A G T G G C T G G C T A C T G A C A A A C G T A A C A T C G T G G C A G G T G G C A A G G G A G G A C A T T T A C A G A A G G T C A T C T C T G A T G T C A C C A G C A G G G C C A G A A G G T T G A T C T G G A G T G G G A C A C A C T C T C T A G A C C T C T A G A C C T C T A A A G G T G C C T C A A A G G T G G T G T A G A G G C C T A C T G C C C T G C C T G G G A C C A G A G C A T A G G C C T T A G T C T C T C T G G G A C A G T A A A G G G C C A C C A O C A C A G A A A A T G C C T A G G T C T T A G C A A G A G A G A A A G C A T C T T C A T G G C A G G A A T T C T T C A T T T C T G T G T T C T T A G G T T T G T G C T G G C A T C A G T C A A C T C A G C C C C T G T C C C T G A T C C A G C A C A C A T T T C C G T A A C T A C C C T C T A G A A G T C A T G C A A A G A G A A A T G A T G A G G A C C A A C A G A A T T A C T T G G C A T C A G G G T T C T T A A A C T A T T T C T G C A G A A C A T T A G T A A A G T T T A A T A A G G A T C A G G C T A C C A G G A A T A C A G T A G G A A C A T G T G G A T G A A T A T T C T T T A G T A G A G G A C T T C T A A A G G C T A T A A T T T G G A T A C A T T A G G C T C A T T A T G A A T C T C A A A A G G A G C A T G T A G T A G G C A T A T C T A A
WI-10778	62	A G	G G G A C A C A C T G C T C T A G A C C	C T G G T G A C A T C A G A G A T G G A C T T G A G G G A C C C T G G G A	C A G T G G C T G G C T A C T G A C A A A C G T A A C A T C G T G G C A G G T G G C A A G G G A G G A C A T T T A C A G A A G G T C A T C T C T G A T G T C A C C A G C A G G G C C A G A A G G T T G A T C T G G A G T G G G A C A C A C T C T C T A G A C C T C T A G A C C T C T A A A G G T G C C T C A A A G G T G G T G T A G A G G C C T A C T G C C C T G C C T G G G A C C A G A G C A T A G G C C T T A G T C T C T C T G G G A C A G T A A A G G G C C A C C A O C A C A G A A A A T G C C T A G G T C T T A G C A A G A G A G A A A G C A T C T T C A T G G C A G G A A T T C T T C A T T T C T G T G T T C T T A G G T T T G T G C T G G C A T C A G T C A A C T C A G C C C C T G T C C C T G A T C C A G C A C A C A T T T C C G T A A C T A C C C T C T A G A A G T C A T G C A A A G A G A A A T G A T G A G G A C C A A C A G A A T T A C T T G G C A T C A G G G T T C T T A A A C T A T T T C T G C A G A A C A T T A G T A A A G T T T A A T A A G G A T C A G G C T A C C A G G A A T A C A G T A G G A A C A T G T G G A T G A A T A T T C T T T A G T A G A G G A C T T C T A A A G G C T A T A A T T T G G A T A C A T T A G G C T C A T T A T G A A T C T C A A A A G G A G C A T G T A G T A G G C A T A T C T A A
WI-10828	23	T C	C A T C T T C A T G G G C A G G A A T T	---	T A T G C C T C C C A C G A G C C A T C C A C G C T C T T A G C A C A A A A A A A T A G A A T A C A T C A T T C T G A A T G G G C A C A T T A A T C T G C A G G C T C C G C J T T C T A A G T C A C C T G C A G T A G G T C T G C A G A C A C T G T G T A T A C C A T A A A T C T G A T T C T G A C A G G A G G G A G G C A G A T G A G A A G G G C T G C T C C G T G A A A T A C T A G T C G G
WI-10832	91	G C A G G C T C T C	C A T T A A T C T G C A G A A T T A A C T G T T C A A A A G T G T G T T A A T	C C T A A C T G C A G G T G A C T T A G A A A T G G C C C T A T A A A A T T G G T A T T A A G	G A T T T G A G T A T T A C A A A T T G C C C A A A G A C C A T T A A C A A G A T T A A T A G T T A A G C C A A A C T A T A A A G A A T T A A C T G T T C A A A A G T G T T A A T C T C T T A A T A C C A A T T T A T A G G G C C A C C A T T A A C T T C T G A A G A A A G G T C A G C A T A T G C A A C T A A A T T C T A A G T C C A G T G G A T G A T G T T C T G T G G T C C C T T A T C J A A A G C C T C T T G C A T C C C A A A T G T G T A A A T T A T T T A T T C T T G G T A T T C T G C T T A C C C A T A G T C A C C T G T C A A G T G T C C A C C C T
WI-2287	24	T C	---	---	T G G T A T T C T G C T T A C C C A T A G T C A C C T G T C A A G T G T C C A C C C T

WI-2296	81 A G	TGTTACTTTGA TTCTTTGCTCT	GCAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGTCTCAGGCTTAGAATAAGTTGTTACTTTGA TTCTTTGCTCTGAC/GGCCAGTTAGCTGTGTGATTTGCAGAGGTTACATTTGTTTGTG
WI-2300	77 G T	GGCACAGAAG CCAGTCATAC	GGTTGGGICAA TTTTAAAGCA	TTTCATCATGCTGTCTTTCCCTGGAAATTTCTTTATTTGAGCGGGCAGGTGGTAGGCACAGAAGC CAGTCATAC/GTTTGC TTTAAATTTGACCCCAACCATTAATAAGAAATAGCATTC
WI-2371	55 G T	GTCTTGTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCAACATTTCCAGGGAAGGTCTGGTCTTGTCTTCCAGCTCTTGGTGGTGCT GTCAATCTTTGACATTTCTTGTCTTGCAGCTGTATAATCCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCCGTGTGTGTGTG
WI-2395	122 A C	GAACATATTT GTAGAAAAAT TACTATCCAA	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGGCACAAATTTAGCTACAGTGCATATTAAGAGATAACATAGATAATCAATAAATGTTTAC TGAAATCTGAAACCTTAGGATGAGTGAACATATTTGTAGAAAAATTAATCTATCCAA/GCJCTGAATTC AGAAATAATAGAAAGGTGAATCATCTTATATCATTAAGAAAGCTAAATTTAGTAACAATCTTTA CATTTACACAAACCCA
WI-2437c	192 G A	---	---	CACGAGCCACCACCCCTACAACCTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATTCCTAAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTG/GA/GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 G A	---	---	CACGAGCCACCACCCCTACAACCTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATTCCTAAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGAC/GA/JAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 G A	---	---	CACGAGCCACCACCCCTACAACCTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATTCCTAAATG/GA/JCTC TAAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 G A	GCAACCTACT GACAAATTTAA TTTTAGTT	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTTCTTAGACCCCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTTG/GA/JGTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123 T C	TGTTTAGGAA ATAATGACAA GAAAAA	TGTTTACAAC GTACCAACAT G	CTGTAACCTACACACATCCTCTGTAACTCTAGGTTACTTGTAAACAAACACAATGTAAATGCT ACATAAAATAATTGTACATACTATATTGTTTAGGAAATATGACAGAAAAAGCC/T/CJGTACAT GTTTGGTACAGTTGTAACACAGCCATTTTCCCAATAATTTCAATCCACAGTTGGTTTAAATCCACAG AAACCACGAATG
WI-2886	46 C A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGTGCAGCCGTTGCAGAGTCTGGGGGAGAAAG/C/AJACGAGATAAAGCATG GCAAGACCCACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTGAGAAACAGAGGAGCGTT

WI-2906b	77 T A			... CCTAGAGTTGGTTGCTGACCAACAA	CCTGAACACCTGGAGCAGCTCCCTCCCTGGACACCTTCATTCTTCTGCTGGAACCTTTGCTGGAAATGCTCTTTCCCTCTT/AJGAGCCTTTGCTGGCTAGCTTTTCTTTTCTTTAGGTTTCAGCTTCAAAGTGACCT
WI-2906a	50 A C	GACACCTTCAT TCTTCTGG		AGAGCAITCCA GGCAAAGT	CCTGAACAGCTGGAGCAGCTCCCTCCCTGGACACCTTCATTCTTCTGCTGG/AJGACTTTGGCCTGGAATGCTCTTTCCCTCTGAGCTTTGCTTGGCTTACTTTTCTTTTCTTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTGCTGACCAACAA
WI-1736	175 C T			...	TACTCCTCATTCTCCTCATGTCCCTAGACGTACTCAGATTTCCATGCCCTGAAACATTTATTTCCTAAATAGATTTCCACCCCCAGCAGCTATTTACAGAAACAGCAGTGGAGCAGTTTGGAGTCTGGCTCTTAGAGAACTTACTTAAGGACAGTGGTTTCCATCTGTCTCTCCA/C/TJAGAGATCTAGGGTGTCTTTTGGAAACCACCTTGG
WI-1851	136 G A	GCATTGAATT AACTATAGAT GTGTTAAGTA		CACTAGCAATG TTAACTGAAG TTG	AATACCCACGCTCCTAACACCATCACACTGATCATCAATCAGGTTTTAACATATTATCTGGGGAGGACACAAAGATTTAGACCATAGCATTGAAATTAAGTATAGATGTGTTAAGTAATTATTAACATGGTACA/GAJACAACCTCAGTTTAACTTGTCTAGTATCCATGTGGATACCATGTACCTTCTTACATCATGTGA
WI-3000	62 G A	CCCAAAACAC AGAGACCCC		ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCAGCTGTCTTACATCTCTAAATGTGAGCACCACCAACACAGAGACCCG/GAJTGAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCGTGGTCATAGTAGACACT
WI-1754	177 G A	TTTTCTCCCT CTTAAAGAGA TAGTC		AAAGTCGAATT GCCTCTGG	ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACTTAAGGGTTTAGCAAAATTCACCTGACAAAGAGTAGGTTTCAACATTGACCCCTCATAAAGTGATTTTCTCTTTCTGTTTGTCTTCTCCCTCTTAAAGAGATAGTC/GAJCCAGAGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37 T A	AAATTC AAC ACAGATCTAT TAGATT C		TGTGATAGTTT TGAGATGGTG	ACAAACACAGCAAAATTC AACACAGATCTATTAGATTCTT/AJACCCCATCTCAA AACTATCACATCAAAGAAGCAAGGAGACATATTACTGTGTAGGAAGCCAAATTCAA
WI-3208	140 G A	GTGGAGTGGGC AGATAAAGA		TCACTCAAAC AGGGCTTG	CAAGCACACATTCAAGCAGTGGCAGGTGGGAGGTGGGCAACTTGGCAGCAGAGAGAGGAAGAAAGTTTCAGACCCGTTGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGGCAGGTGGTGAGTGGGCAGATAAAGA/GAJCCAAAGCCCTAGTTTGAGTGACACTGTGGGGATTCAAG
WI-1775	47 C T	CCTGCATGGTC TTTTCTCTG		AGTTGAGATT ATGACAATGAT GTAA	ACTCCACCAACAGTTTTGTGAGCCAAACCCCTGCATGGTCTTTCTCTG/C/TJTTACATCATTTGTGCATAATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55 G A	AGCATATTCA TTGATTTCCCT ACAT		GAGGACTTAA AAGGAGCATTT G	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCAATTGATTTCTTACAT/GAJCAAATGCTCTTTTAAAGTCCCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAATAGATTCTTCTTAGGA

WI-3416	33	C T	CCAAGTTGTA GCATTCAGAA	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCCTCCAAGTTGTAGCATTGAGAGTCTCTCTCTAGAGGTAGTTGTGCTCGTCTGTTAAAA TATGTTTCAAGATAGTATCTCCCTGTTGTACCTTCTCCTCAACAAGTGTACCAACAGCATTTGTTAAG GAAATGTGCAATGCTTGTCTACCTCTGACGACACACATAATTAATCCCATTCCTAAAAAGACCAGG
WI-3453	70	C T	TTCTAGGCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCTACAACAACAGAAATTTAACAAATTGAAATCAGCTACTCTCTTCTTAGGCCCATCAGAG AATCTGGAAGTCATGGGAAATGATGCCATGTGAATGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACAGGGACACAATCCACTTCCAGAGCCCATCTGTAAAGAC
WI-3474b	109	G A	CATGCTAGGTAGTCTGATCATGAAGTTTGAACAACTTAAATCATCAAGTGTGCAACTGGTTTGA GTCAGTTCCCTAATTTAGCACAGTATTTAATGAGGTGGTGGGAGAAAAATTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90	A G	AGTCAGTTTC CTAATTTAGC AC	CAACCATCAAT TTTCTCCA	CATGCTAGGTAGTCTGATCATGAAGTTTGAACAACTTAAATCATCAAGTGTGCAACTGGTTTGA GTCAGTTCCCTAATTTAGCACAGTATTTAATGAGGTGGTGGGAGAAAAATTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3502	79	C T	CCTGGGTTTCT GGATGTCT	GGGTGAOCTG TCCTCA	TTTGACCCCATACATGAGAAATAAACCATAGAAATGGTGGAAAAATAAACGGGAGAGACCTGGG TTTCTGGATGTCTCTTGGAGACAGGGTCACCCAC
WI-3600b	146	G C	GGTTTCTAAC TGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGTACTCTGCTGTTTCCAGAGTGTGATTATCCATGCCCCCTG ATAGTTCTGTGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGTTCTAACCTGGATA TAAACATCTGATGGAAGGCTGCACTGGATGAGGTACAAA
WI-3600a	78	T G	CCATGCCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTTGTACTCTGCTGTTTCCAGAGTGTGATTATCCATGCCCCCTG ATAGTTCTGTGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGTTCTAACCTGG ATATAAACATCTGATGGAAGGCTGCACTGGATGAGGTACAAA
WI-3678	125	G T	TAAATCATGCTTATTTTCAACAAGGTAATCCACTCACAAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAGCTCTCATGCTCTTCTGAACTTCTACTTACTGTGCTGTTATGATGCACCTGTTCTTTTGG ATAGATGGTTGATAGGAGATGGTTGTTAAAGACACAATTTACCTTGTGTTTTCAGGCAGAAATAG ACTCTCTGTGTAAATCACTGAATGAGTCCAAAAGCCTTATGTCTTAC
WI-3687	67	A C	AAAGCGATGTTGAGATACCACATCCATGAAAAGTAAAACACACACACACAAAATATGACATAAAA TTC/AAAAAATACTATAGTTTATGAAAAATGACTTCCAAAATTCAGAGAAAAGTCACTTAAACAGG ATTCTCAATTCAATCCAGAAATCTCTCTGTCAATCTTAACTTTGACTGCACAG
WI-3735	72	T C	CCTCAGTTATG TATCAAAATGA AAAC	GGCTCACCAT CATTGTTTT	TCATAAATGTGAAACCAAGAAATCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAACTTC/ACACCCGGTTCAATGAAAAACAATGATGGTGAGCCATGTCCCTTATTTAATGAAAA GATCTTGGGCAATTAAGTC

WI-1819	51 C T ---				GAAAAGCAGGAAGCCAGGAGGACAAACTTTTGAAAAAGTCTTTTCAGCAC/CJTTCGGGATCCG AATTTTAGTGTGATTTGGCAGGCAATGCGGGTAACATGTTCCAGTGTTTTAACTTGCACAGAAATGC CAGATTAGCGATTGTTGACTTGTCCTCAATTAATGAAATGTGGAAAAAAGGGTGGTAACTGTT AAGCCTGCTGCAATGTTAGACACGAGGGTGGGGAGGTGAATACC
WI-3746	118 G A ---				GGCCTATTACATGACACTGGGCAAGATCTTGCTTCCCTTTCTTTCATAGATAGACTAAGTAA ACTGCCCTGGCCAGGAAGATGTTGTCTTCATCATCTCTGCTCTG/CJA/BCCCCAGGATAAAGCA GGCA
WI-3867	49 T C C A A	ACAGTCATT AGTCTTCTGA	TAAGATAACC ATACTAGGTAC ATCCG		AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGACAAAT/CJCGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAAGTGGAAGCCAGCATTTCTAATCAGGCTCAGTGATCTGCCAAACCAACCTTCTGCTATAG CATC
WI-3898	25 A C G	TGACCAATGTC TTTAGAAGCA	TCGTGGTGTG CTCTCC		CAATGACCAATGTCTTTAGAACGAG/CJGGAGAGGACACCCAGCAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGACCCACAAAGGTGAGGAAGCAAGGTTGCTGGCCACT
WI-3901	114 A G ---				GGACATTGTCCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAACTCGGCTTCTCACCTGACAAGTG/CJATCATGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	99 C T GC	TGATTCTTCTC AAGACTCACA			CTGAGGAGATTGATGCTACTTTACCTGAGGAACTTTTATTACCTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATTCTTCAAGACTCACAGC/CJACCATGCTTCTTCTAGACCTATAACTAG ACTCAAGTCCAGCAGGCCCTTAAAGGTAAGGTACAAAGTGTGACCCATGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33 G A A	CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG		CCACTCCCAGGCCAAGAGCGTCTATGAATCAT/GJA/CATTGTTTCTGTTATTGCTGTTACACAGAT GGCAACTCTTGCAAAAGGGAGGGGTACAAAGTGAAATTTTAGATGCTGCAGGAGACGAAGGTC
WI-4091	84 A T	TTGAGGTCTTA GTCAATGCAATG	TGAGTTCCTAT TAAGTGACAAT ATTGTT		TAATTCACATTGCTCTGTTGTGCAATTTATTGCTTCTTATGTAAACACAATCACCAACATTGAGG TCTTAGTCATTGCAATG/JATJTGATAACAATATGTCACCTAATAGGAACCTCAAGCATAGTTATGTT ACATTTATTGCTAACAGCAG
WI-4160	117 A G CAACAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGOC		TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCCTTTGAGGTTAGGTTGGCTTCTAAGATGGTAAT ATCTGTCCAAGTTTTTGTTCCTATAATTTAGCAACAATATCAACAGAA/JG/GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATCT
WI-4168	32 A G AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA		CGTTGCTGGTGAGAGTCAAAATTGATACAAACA/JG/JTCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAATATATACCAGCAGTGGTCTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT

[illegible]

WI-5204	54 C T	---	---	TAGATTTGATTGATGACAATAGGGAAGCCTTTGTTAAATTTGGGTTTGAAGAA(C/T)GAAGAAAA TGGAAGGGGAAGATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAATCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70 A G	CTCAAAA	GGACCTTAAT ATTAACAGA TTGCG	TTTCCCTTATTTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATAATTTAACAGACTCAAAAA TATAGJGCGAAACTATCTTTACAAAATTTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112 T G	ATATAA	TTGTATCAAA GAGATGGGGT GTTCTT	CCCTGAAATGTGCTTTGCTTCTCTCCACTCTCTAGGGAACCTTTTCCATGTGAGGTGAAGGTTTTGA AGAGTACTTTAATTAACTTGATCAAAAGAGATGGGGTATATAAT/GJAAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTCATCAGGGCTCTTCCACTGTCTATCAGTAA
WI-4456	49 C T	TATAGTCC	AGTTGAATTA TTCAGAAAAT GCATGAACCTG	ACACATTTTCTTGTCTTAAGTTGAATTAATTCAGAAAATATAGTTC(C/T)CAAGTTCATGCATAA CAGGAAACACCCAGGTTGGGCAATTGATTGAATTGT
WI-4461	49 A G	CCCTCC	TCACTGTATT TTAAAAATTAT ACCAATTTCA	CTGAACTAATGAGGTGCTAAATCACTGTTATTTTAAAAATATCCTTCC(A/G)TGAAATTTGGTGAAA GGTCAAGAATGAATCCACTTTTAGATTTCTGGAAATTTTATTTGCGATGATAATGCAATGGGC CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGTATATAAAGAAAACAGTTAGTAATCTT TCACCTTT(G/A)TATTCTCTTCTACCTCAGGGAATC
WI-4465a	41 A G	ACACGAAAGT	GGTGAAGATT ACTAAGTGT TCTTT	CTACTGGATTTTACTTTGCTCAAGCCAGACACAGAAAGT(A/G)TATAAAGAAAACAGTTAGTAAT CTTTCAOCTTTGTATTCTCTTCTACCTCAGGGAATC
WI-1949b	160 T C	TAATC	GAGTGAATAA ATGAATGCCA GACAAAA	GGGTTAGGACCTCGAGATCTTTTCAAGAAAGCACAAATTCAAACCAATATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT(G/J)CAAGGCTGCTGACATGGTCAATATATATGTTGAAGAAATAA GGAGTGAATAAATGAATGCCATAATCT(C/J)CTGTGTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-1949a	86 T G	ATGCTGAGT	CAGTGGTGAG GCTTG	GGGTTAGGACCTCGAGATCTTTTCAAGAAAGCACAAATTCAAACCAATATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT(G/J)CAAGGCTGCTGACATGGTCAATATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-4529	64 T C	AAGATG	CCAAGTAAGT CTATCATCTG AAAA	TGAGAGAGTTTTGGATTATTCATCCTCTGCAACACTCCAAAGTAAGTCTATCATTTCTGAAGATG(T/C) GAGTTCTCTTTATATCCTATGATATTTTTCAGGAAGTGTATTTTGAATATAAACTCCTGGGT CCCATCCAGGTTAGGGTCAATGGCATCCATGGGTGCTGGACAAGATGGGCCCTAGGATCATTTT

WI-4540	110 A G	GCACCATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTTCCTTTTCTTAAATTTGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCACCATGTGGCATCCAGTGCATGGCTGCATTTGCCAGTC AAATGAGACAACTTCCTAT
WI-4582	226 T C		---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAAATTCACCAACACACACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTTAACTTATTCCTGTACACA AATAACTTTATGGGAGACAGCATTGTAATTCAATCAATAATAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTT/CJCTCTTGGTAGAAACCATTTGAT
WI-1965	105 G C	GCATGAGG AAGTGTAA	GAATGGATGGG TCACTCTCT	CAAGGTTAGTTTAACTTGGGGGCAACACAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTGTAAAG/CJAGAGAGATGACCCATCCATTCTCTGG GCTTCTTATATGACACCATACTATTCCACACAGATGTGGAGTCATTTATTTGGTTGGTATGACAGT CATGG
WI-5248b	99 C T	TTG	AGAAAAGAG AAGAAGGAA AAA	TGTTTAAACCATACAGTTTGCTGCTACGTTGTGTTAGAGCAACCCAGAAAATTTAAACGCCTAC CAITTTTCACTGTTTCTATTGACCGTACTTG/CJCTTTGCTTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTAACTATT
WI-5248a	38 G C	CTACGTTGTT	TTTTAATTTTC TGGGGTGTCT	TGTTTAAACCATACAGTTTGCTGCTACGTTGTGTTAGAGCAACCCAGAAAATTTAAACGCC TACCAATTTTCACTGTTTCTATTGACCGTACTGCTCTTTGCTTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTAACTATT
WI-4596	69 T A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTGGTGACATTACTCTGTGACTTGTCTGAAGCAGAAAAGCACTGTGA CT/AJCAATTATAGGCCCATCTCTGCTGAAGCCTGCTGACAGCAATTTGAACATATGGCATTGGG ACATATCTCTGAGCCCATCACTATTGACAAGATTCTCTTTTTTAACAA
WI-5252	119 A C		---	GAAATAGGCAAAATTAAGACCTTCAATAATTAAGAAGCTTGGGAAAAGGATTTGTGATGATCATTTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTTGCTTT/AJCTACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61 A G C T	GCAATGCTAG AAAATTATGC	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAATGATAACCAGGACTGTTGTTCAAGCAATGCTAGAAAATTTATGCCTA/AJGJC CAAGTAGACAACTTAAGCACCTAAGGCAGAAATGAAGTTTCTCTTGTCTTAAAGTCTCTATTCA ATTACCATTTATCGGGTAATTAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGCTTTGCTATGCT
WI-5257	77 C A	GAGGCATGAA GCAAAGAGG	OCAGGGGCAGA TGAAAG	CAATGAGAAAGTTACCAGATCGGGGCAAAATTAAGCATATGAAATACCAAGTGTGGCAGAGGCATG AAGCAAAGAGG/CJCTTTTCATCTGCCCTGGTGGTTTTTCAGTAACCTGCAACATGCTTTGCTCTOC CGGATGAAAGATACCCCTTCTATGACTCAGCAATCCACTCTAGGTATGCACCCTAAACATGGGTG GCAAAAT
WI-4649	50 C T	TTCCGAATG	TGTACTAGGTG TACTTACAAGA AATCATC	TCACCTGTTAGAAATTTCTTCTCTCAGTGAGACCATCTTTCCGAATG/CJGATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAAATTAACAAGTACTTGTCTACCTGAATTTGATTTTTTAA AAATCCTCCCAATATTG

WI-4650	148	A G G T C T C T T	GCACAAAGAA AGTATAAGTT	CTGAAGTGTTA AACTGGATTG G	AACTGTGGTATGATGTTGTTGTTATTTTCTGGAGAGTCAGTTACTCTCAGTATCATAAAGGG GACTTGGAAACCAAAAGTATCTCAAGACATTTAATCTAGAACACAAAGAAAGTATAAGTTGTCTC TTATATTGCTTTTJAG/CJCCAAATCCAGTTTAACTTCAGTAACGTT
WI-4677	82	T C A A A	TCCAAAAGTG ATTAGGTGAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTCGACATTTTGGAAAAAATTTGCAAAAAGTATTAGGTGAAAAAT GAGTTGAAATAAATGTC/JAAGTTGAATAATGACACTGTTGAAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C G ---	---	---	ATGATGCTATCATGAGGAATCTGTAGAAAATTTTCACTGGCAATTTGATTCAAAATAAAGTTTGTC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTTGTGACGGAAGAAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCGCTGAAGCCATTCTG
WI-4722	88	G A A A C A C C A C A C	TGCACTATGG TGCATTGAGTT	AATATGGAATC TGCATTGAGTT G	CTTCCCATTCTGCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGGAGATTTATTTTC TGCACATATGGAACACCACACG/AJCAACTGAATGCAGATTCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C A ---	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGTCAGTAAATCAGTTTGATGGTTGAGATTTTCAAGAAACGTGAAATTTATTGAGTAACCATGGG TCAACTATGATC/AJCCAAAACAGCAGTGTTGTCTAAAAAATATGATAGTTTCTCTCTGTCACCC GCAATGAAAAGGAGTT
WI-2028	176	T C C C T G T C T A T C	TGTTACGTTT CCTGTCTCATC	GGTTGGAACT CAAAATTACCTA GAA	GACTACAGCGCACAGACAGGCAATTGTGTGGCTTGACAGGTGTTGGTTTGTGTTTAAAGTTAGATT TGAATCCTTTAAAGAAGAAAAGTGCTCTTCAGTTTACTACAGACCTCATCTCCTGGTTCTCTTG CACCCAGTCCACTTCACCTGTTTACGTTCCCTGTCTCATCTC/JTTCTAGGTAATTTGAGTTTCCAACC TGTTGG
WI-2033	183	T C A	GGGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTCC	ATGTTGTATGAGCTCCACATTTCGCAGATTCAACCACTATGGATAGAAAATATAGTATTTCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAAATTTTAAATTTTCCAAGTTTATACAGGACCAGTGTGGAAATTT AGCATTTCTGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA/TJCJGGAGAACGTGGAAACC ACTGATATACCAAT
WI-4745	131	T C ---	---	---	TTATGGATACATGTTTCTGTGTGAAGGACAAGAGTTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACACAGGCTCCTTTCCACCATTTCTCCATCTCTACTCTGAT/CJ AGGCAGACTTATATGAAAAAAGGGA
WI-2034	150	T C C A A G G A C	CCACAGTGCA CCAAGGAC	GGGTAAGAT AGAGTGCAGGT CC	CCACGACTATGTTCTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATTGTGGCCCAAGA CCTCCTTCTGCGGTTTCAAGTGAAGACGATGAACCTCTTCTACAGCAGCTGAGACTTCACCA CAGTGCACCAAGGAC/TJCJGGACCTGCACCTCTATCTTTACCCCTTCCGACACCAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	CT	TGTCCTTTAA GTGTGAAGT ATTAATTAG	ATTCTCTTG AAAGAAACAT CA	TCAGGTGACAAGAAAAGTCACATTTCTTCAATCACTCACCATTGCTGTTATTGCTCTTGCAAGTGT ATCCAAGGATGTCACATTTTGGAACTCTGTAGATCAGAAAACTGTGCTTTAAAGTGTGTAAGTATTA ATTAGATTCTATTTTGATA[C/T]TGATGTTCTTTCAAGAGGAAAATTGTGTAAGAGATTCCCATTT TGCAATTCATTGGC
WI-4782	113	CT	GATCAGAAG ATAACTAGAA AATGC	GAACCTCTCTG GTTATTTTCT GTTC	TCATTGACTTTTAGAGTCTCTTCAGTCTTTATGCTCTTTATGCTTTAGGAAAACTAGGCTAGGAGAA CACAATTCAGGTTCTCTCCAGATGCAGAAGATACTAGAAAATGC[C/T]GAACAGAAAAATAACCA GAAGAGTTCAATTATGTTTTCAGAACGATTAC
WI-4788	65	AG	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAATT AAAATTTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAAITTCAGTGCATAGATCATCTTGTAAAGTTCC[A/G] JTGAATAAAATATATGCCAAATTTAATTTATCCAAACTTTAAGTCGAGATTATAATTGATATTT AAAAACTATATTGAGTCTTTCTTAAAGATGGCGTATCACTCTA
WI-5300	38	TC	TCCAGAGAC CACTTCATTC	CTACTCTTTCT ATTCATAATC CAAAA	CTTACTTCCAAAGTGTTCCTCCAGAGACCACCTTCATT[C/T]TTTTTGATTATGAATAGAAAGAGT AGGTGTTATTATCTCTTTTACCAGGTGAAATTTGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGACAGGCCA
WI-4818b	121	GT	TGATAATGGG GCCCTGTT	CCCTCCTTTTA TATGTATGCCA GA	TATAATGTTTGTTCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAAACAACTCTTATATA ATAATTTATTCAAGAAGGAAATATACATATGGGTGATAATGGGCCCTGTTG/TCTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43	AG	TTGCCATAGAC TAGGTTATGTC C	CATATGTATAT TTTCCTCTTG AATAAATT	TATAATGTTTGTTCATAGTTGCCATAGACTAGGTTATGTCC[A/G]CACATGAATAAACAACTCTTAT ATAATAATTATTCAAGAAGGAATATACATATGGGTGATAATGGGCCCTGTTGCTCTGGCATA CATATAAAGGAAGGCTAA
WI-5317	139	TC	TTCCATTCTG GTAGCAGGT	GATGCAAAGA AGAAATGAGTC C	TTTTTCCATTTGTTGATTCCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATATGATGTTATATATACAAATTCAACTCAACAGGAATCCATTTCTGTGTCAGGT ATA[T/C]GGACTCATTTCTCTTTCATCTATTTCTAGGTTATTTCAGCCCGGAGATCTACCCAGG
WI-4888	56	GA	GCAAGATATA AAGATTAGA AAAGATAACA	CAATTCACCTA CCTCATTTATT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAAATTCCTGATACTGGAGTAGTGCTT
WI-5328	44	AG	---	---	AACATTTTTTAACCATGCTACATTTACAACACTGAAAAGACAG[A/G]AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATACTGGAAGGAG
WI-4897	93	AG	---	---	GCCTTTTGTAGTTAAGTCTTTTGTAGTGTGCTTTTTTTTCCCCACTAGTACTCTCGGGCCCAAT CCCCAAAAGAAAAAAGCGCTTGG[A/G]GATAAACACATCTTC
WI-5345	29	GA	---	---	CCCTGCTATAGGTGAGTTTAAAAATCCT[G/A]CCTGCTATGGTTTGTGTTGAAGCCACATCCACT GAGGTATATTCTGTCTGCATTTTCTATATCACTCAGCTTCAGATCCACTCCATCAACTTGCAG

WI-5370	143 T	AATAAGATGG TACCTTAACCTA	CAGAATTTG CAGAGAAATTC	CAAGTTGGTA CAGAGAAATTC	TGCATGTTACTTCTTGGAAATCATAAAGGGATCTGAGAGCCTACAGTATATGGCAACATTAAACCAAT CTTTTGAAAATTTACCTGTATCCCATCATGGTTCAATTTGCAAAAAATAAGATGGTACCTTAACCTA ATAAAACAATTCCTTGAATTCCTGTACCAACTTTCCTTTTC
WI-9711b	423 T A	---	---	---	GATCTCCTTCATCCCTCTCCAGAGAGGAGAGAGAGAAACACAAGAAACGCCTGGTGACAGAGCC CCAATTCCTACTTCAATGGATGTGAATGCCAGGTGAGGAGAGCGCTTCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTGTAGCTGTCTGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9711a	390 C A	---	---	---	GATCTCCTTCATCCCTCTCCAGAGAGGAGAGAGAGAAACACAAGAAACGCCTGGTGACAGAGCC CCAATTCCTACTTCAATGGATGTGAATGCCAGGTGAGGAGAGCGCTTCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTGTAGCTGTCTGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9702c	345 G A	---	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCGCTCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGACAGGTGCCCTCTGTGCTATTCAGCAATCCCTACTGCTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATCTAACTTTAATGATCTCTGTGACTT TTATACCTAGCTTTAAGAGGTTTTCATTCAGGTGCTACAGCATCTGATAG
WI-9702b	344 C T	---	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCGCTCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGACAGGTGCCCTCTGTGCTATTCAGCAATCCCTACTGCTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATCTAACTTTAATGATCTCTGTGACTT TTATACCTAGCTTTAAGAGGTTTTCATTCAGGTGCTACAGCATCTGATAG
WI-9702a	179 C T	---	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCGCTCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGACAGGTGCCCTCTGTGCTATTCAGCAATCCCTACTGCTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTTTATCTAACTTTAATGATCTCTGTGGA CTTTTATACCTAGCTTTAAGAGGTTTTCATTCAGGTGCTACAGCATCTG
TGR- A003N21	49 C A	---	---	---	TATAGTATTTAACGAAGCCTAGAAGCAGCGCTGTGGGTGATTTGGTTC/AJAGCATATCTTAGGT ATATAATACTTTGAAGGCCATAACTTTTAACTGGAGTGGTTGATTTCTTTTAAATTTTATGGGA GGGTTTGGATTTTAACTTTTAAATGTTTAAATATTAAGTTTTTGTAAAGGAAACCATCTCTG TGATTACCTCTCAATCTATTGT
TGR- A004V30	203 C T	---	---	---	AGAATGGCTACTTTCATAGGGCAGAGCAGCCACTTTTGGCTAAATTTTAACTCCAAAGCTAATAAT AATCAAGAAGAAATAGAGAACATTAAACAAATAAATATGTTCTATTGGGAATACCTAATATCAG ATACTAACAAAGTACAGTGATAAGAAATAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGC/G.TCTTCTAGGTTAGTAGAAAGTT

TGR- A004W22	232 C A ---	---	GGATAATCAGTACAATAATGGGACCTTAAACTGCTGTGATCGAGGAGTGAGGGCTGGGCAGTG CCGAGCGAGGGGAGGACAGTGGGACAAAGGATGCTCAGTGGTGAGCCACAGCCCTGGGCTCTGGA TGGGCATGGGAATGACCAGGTTCCACATCATGACAGAGGGCCCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTGGTGTCTGCCCCCGCCTA/CATCTGGAGATGTCTCTAAAA
TGR- A005D24 b	138 C T ---	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAAATCTCTTGAGATAATTGATTTTCATATTG TGTGGCTTCAACCTCCATTACCTCTTGTCATCCACATCTTTATAGAGAAATAAAAACCCCAATTT CTC/TJTTTCAACCATTTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAGGAAACAAT
TGR- A005D24 a	123 A G ---	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAAATCTCTTGAGATAATTGATTTTCATATTG TGTGGCTTCAACCTCCATTACCTCTTGTCATCCACATCTTTATAGAGAAATAAAAACCCCA TTTCTCTTCAACCATTTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAGGAAACAAT
U03735	74 C G ---	---	TGAGTCTGAGCACGAGTTGCAGCCAGGCGCAGTGGGAGGGGCTGGGCCAGTGCACCTTCCGGGGCC GCATCC/C/GJTTAGTTTCCACTGCCCTCTGTGACGTGAGGCCCATTTCTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGGTTTCTGTTCTGTGGATGACTTTGAGATTATTCTTTGTTTCTCTGTTGGA GTTGTTCAAAATGTTCTTTTAA
U39840b	42 T C ---	---	GGTTTGTCTGGCATAGCCATGCTGTGAGCAAGAGAGAAAAAAT/CJCAACAGCAAAACAAACCACA CAAAACCAACCGTCAACAGCATATAAAATCCAACTATTTTATTTTCACTTTTTCATGTCACAACCC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTGATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTTTC
U39840	56 A C ---	---	GGTTTGTCTGGCATAGCCATGCTGTGAGCAAGAGAGAAAAAATCAACAGCAAAACAA/CJACCACA CAAAACCAACCGTCAACAGCATATAAAATCCAACTATTTTATTTTCACTTTTTCATGTCACAACCC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTGATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTTTC
WI-8997	41 G A OCCC	GGCCACTTGCT AGTGCTCA	GTGGCCATCGATCTGGACCTGCCCTGCCACTTGCTCCCG/GJTGAGCACTGCGTACAAACATCCA AAAGTTCAACAACACACAGAACTGTGTCTCATGGT
WI-7008	180 A G ---	---	TATACCACCTTCCATTGATGGAATGCTGCTGTTCATGACCAACTTTATGGCTAGATGGTGCAGAA AGCACCCAGTTTATGATAGGAGTTCAGTGCATATGGTACTTGTAGTCCAGAGTCAAAACATTTCAG TTCCACCAAAAGCCAGTAACAGGCCAAGAGTGTCTCTCAAAAG/GJAGAGTAGTTATCTGCAGA AGATGGCAGGGCCTTGCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACT
WI-8005	26 C T GGGATCT	CGAATTTGCTG AAA	GGTCCCACGAATTTGCTGGGGAATCTC/TGTTTTTCTTCTTAAGACTTTTGGACATGGTTTGACTCC CGAACATCACCGACGGTCTCTCTGTTTCTGGGTGG

WI-7593	46 G A	TTTGTGCTCTGGACACCCACTGCTCCAGGATGAAGGAGAG/GAATGAGATCAGTTTGGACACTTCTCTGAAATATAAAGAATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCTCCAA
WI-6962	78 A G	AGTGCATCTTGGGGAAGGCTCCAGTGTATCTGGACCAGTTCCTTCATTTTCAGGTGGGACTCTTGATCCAGAGA/GGAGACAAAGCTCCTCAGTGAGCTGGTGATATATCCAAGACAGAACCCCAAGTCTCC
WI-7059	43 C G ...	GCTCTCGCTG GGTCA	TGACTCTGCGCTTCTATGCGCTCTATCCTATCATAGATAACATCTCCACAGCCTCACTTCAATCCACCTATTCTCTGAAATATTCCTGAGAGAACAGAGAGATTAGATAAGA
WI-9063	53 A C TT	AAGGCACCA GCCATC CACTTCACTGA AAGACACCAT	GCAGAGAAGAGAACCATGCCAGGGGAGAGGACCCAGCCATC/GGTGACCAGCGAGGAGGCCAACTATCCCAAATATACCTGGGTGAAATATACCAAATTCCTGCATCTCCAGAGGAAAAATAGAAAAATAA
WI-7079	293 T G	GATGAATTGTGCACTCTTAAAAAA
WI-9074	38 A G AAAAG	TCTACTTTCTG CCTTGGGT	AGCAGCCATCATGATCTGTTTTTACCACCTTCACTGAAAGACACCATTTATACJTACCCCAAGGGCAGAAAGTAGAACTTACTATTCAATGTTTGACACAATTGGAATTGTC
WI-7104b	249 C T	AAGGGCATTGAGACTATAAAGCAGTAGACAATCCACATACCATCTGTAGAGTTGGAACCTGCATTCTTTAAAGTTTTATGTCATATTTAGGGCTGCTAGACTTACTTCTATTTCTTTCCATTGCTTATCTTGAGCACAAAATGATAATCAATTATACATTTATACATCACCTTTTGACTTTTCCAAAGCCC
WI-7104	157 C A	TTTACAGCTCTGGCATTTTCTGCTAGGCTGTGAGGTAACCTGGGAT
WI-8974	34 C T AAGAACTCA	GACAGATTTT GACCTAGTTCC TT	TGGATCCGAGGTAAAGTTCTTTTGTCTCTAAAGAA/GAAGGAACCTAGGTCAAAAACTGTCTCCGTGACCTATCAGTTATTAATTTTAAAGGATGTGGCACTGGCAATGTAACIGT
WI-9161	61 C T OCTGGC	...	GGAGTTGCCCCCTCTAAGGGAAGGAGATCTTTATCTTCTGTTGGCTTGACCAGTCACGTTGGGA
WI-9014c	93 T C	GAAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGGTCTACTTTGGACTGAGAGAGGAGGCC
		...	CCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGGCTGGGTCTGAGGAAGCAGATGTTTCATGCTGTGTAGGCTTGCAACAGGTGGGGGCCACAGCACCCAGCAGCATCTTGGCT
		...	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA/GTGGCAGCTCAGCCCTACACCAGTTTCCACCTGGAGTTTCATGCAAGGGCAAAAGGAGTGCCATGCAAGCTGTTTAA
		GCTTACAGGAG	CTGTGAGGGTGACGTTAGCATTACCCCAACCTCATTTTAGTTGCCTAAGCATTGCCTGGC/CJTTC
		AGACTAGACA	CTGTCTAGTCTCTCTGTAGCCAAAGAAATGAACATTCCA
		GGAA	COCTGTTCCCATGCTGACCTGTGTTTCTCCCCAGTCACTTCTCTGTTCCAGAGAGGTGGGGCTGGAT
		...	GTCTCCATCTCTGTCTCAACTTATTC/GTGCAGTGTGCTGCAACTTCT

WI-9014b	44 C T ---	---	---	COCTGTTCCCATGCTGACCTGTGTTTCCTCCCAAGTCATCTTTC/TJTGTTCCAGAGAGGTGGGGCTG GATGCTCCATCTCTGCTCAACTTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206 C A ---	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGGTTTGTGACAGATG/CJCCCTGCGT CAGTCCCTTTAAGTGCATCCGCTGTGCTGACTTTGAGTGGATCAACATCTGCTACGGTCCOC TCTTTTGGCCCCAGTATTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC A/C/AJACACACATCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGGTTTGTGACAGATG/CJCCCTGCGT GCTCAGTGCCCTTTAAGTGCATCCGCTGTGCTGACTTTGAGTGGATCAACATCTGCTACGGGTC CCCTCTTTTGGCCCCAGTATTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAC CACACACACATCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	---	CTGAAATCCCTCTCTGCTGCTGGCTGGATCCGGGACCCCTTGCCCTTCCCTJCTGGCTCCAGCC CTACAGACTTGTGCTGCTGACCTCAGGCCAGTGTGCCGACCTCTCTGGCCCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAAGTTGTGTGAAGCAGAGAGAAAGCTGGAGGAAGCCGTGGGGCCAAAT GGGAGAGCTCTGTATTATTAATATTGTTCGCCCTGTTGTGTGTTGTTA
WI-9171	62 G A ---	---	---	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAAGAAAGTAGAGATAATAATCA/G/A TTCTTTACAACCGATGGTAATTAAGCTTGTTATTCACAAGACTTCATGC
WI-9174	47 T C T	CTAGGACCC ATTCTCCTATT	TCTAGAGGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGTGTAGGACCCCATTCCTCTATTAT/T/CJAGTCTCTGCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAATTGAG
WI-7753	52 A G GAAGAACAGA	CCATGTTCCGA GAAGAACAGA	CAGAGGCTTG AAATACAGGG A	AAGGCCAGATGCACATCCCTGGAGGACATCCATGTTCCGAGAAGAACAGATJAGJATCCCTGTATT TCAAGACCTCTGTGCACTTATTTATGAACCTGCCCTGCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTTCTTAAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A CGCA	CCACTTCTCCC CGCA	AAAGGGAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAACAAAAAATGGCATCACCTGTCAAAAATGGAGTCCACT TCTCCCGCA/G/AJACCTAGGTGAGACTTCCCTTTTCATCTT
WI-9193	94 G A CA	AGAATATTGT CTGCCCTAAAG CA	GGTGTGTGTGG TAGGGGG	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGAATAA CTCAGAAATTTGTCTGCCCTTAAAGCA/G/AJACCCCTTACCACACACACCCCTGTCTC
WI-9015	48 C T ---	---	---	TTTGATTGATATCGTGAATCTCAGCCGAGAAATTTGGGCTGGATTG/CJGCTTTGGTTAATACAT CTTCCCTAAAGAAGATAAACACAAATCCATTCAGGTAGCTCGGCACCACTAAGAA
WI-7254	37 A G AGGAGCCAC	GGTCTGAGAG CATTAGGGA	GGAGTGGGTGT CATTAGGGA	GGAGCCAGGAGACAGCAGGGTCTGAGAGAGGAGGCCACJAGJGTCCCTAATGACACCCACTCCTAGCC CTGAGGCTGTGCCCTCAGACTGGGGAAGAGTCCAAAGGAGGGAGGAGGCCACTCCTCCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG

WI-9231	32 GC	CAGTCCCCA GATTGA	CAC TTGCCAC ACTCAGAC	GTGACCTGTGAGGTGAGTCCCCCAGATTGA/GC/GTCTGAGTGTGGGCAAGTGTGTCAAAGGGGC TGCCCCCAGGAGATGAGGTGAGAGCAGGAGTTGAGGCCGAAGAAGTCA
WI-7836	120 TC	CAAATAAAC ATGCAACGTT C	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTGGGAAATAGAGAGTTGAGATAAACACTCTCATTAGTACTGAAAGAAAACCTCTGCTA GAATGATAAATGTCATGGTGTCTATAACTCCAAATAAACAAATGCAACGTTCC/TG/GATTCTTAAT CTTGGTTCTGAGAGCCATTGGTTTCAGTTGTAGCAATCCCATACACAGCT
WI-7286	65 TC	CAGCTTCAGCT TAACTGACAG A	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTCAGCTTAAGTACAGAT/C JGTTAAAGCTTTCTGGTTAGATTGTTTTCACCTTGGTGATCATGTCTTTCCATGTGTACCTGTAAATATT TTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 TG	CTAAGCATGT ACGTGAATTT TAAAT	CCCAATTTTA TTAAAGTTTA CATCTAT	CAAAATCTTGAAATATCTCAAATGTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT AAGCATGTACGTGAATTTTAAATTT/GTATAGATGTAAACTTTTAAATAAAATTTGGGTGTGG GAAGATTAAAGGAGGTGCTCTGTGGTCTCTCCCTGCTCCCTCTCCCA/C/A.GTGGGGAGAGACC TGTGATTGCCAAGTCCCTGGAOCTGGACCAGCTACTGGGCTTATGGTTGGGGTGTAGGCAGG TGAGCGTAAGTGGGAGGGAATGGTAAGAGTCTACTCCAAACCTAGGTCTCTATGTGCAGACCAG ACCTAGGTGCTTCTTAGGAGGGAACAGGGAGACCTGGGGTCTGTGGAT
WI-7860	50 CG	CGTACCTCAA ACATAATTGA TTC	GC TTGAGTGA AGTCTGCAGA	CAAGGCGTACCTCCAAACATAATTGATTTC/GTATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGGAGGCTGGCTACTGTCTCTCTGCACTCTGCTTTG
WI-9064	29 AG	CGTTC		CACACTGTCTGTCTCAGTCTGAGGTCTGCGAGGTGCGGCTGAGGTGAGCGGGGTCCACA GGGCCAGCCCTGGCAGGGTCTGCCCCCAGTAGGCGGAGAGCAGTCCCTCCCTCAG/GTAACT GGAGGAGGGACTCCAGGAATGGGGAATGTACACACCATCTGAAAGCCAGCTTCACCTCCAGT TTGCACAGGGATTGTCTGGGGCTGAGGGGCTGTCCCAACCCGCC
WI-7307	128 GT	GAAATGTGAC TTCACCTTGGT G	CAGGTAGAAT TTCTGTCCATT G	GAGGAAATGTGACTTACCTTTGGTG/C/TCAATGGACAGAAAATTCACCTGTGCTACATAGGAGAA GTTTGGAAATGCACCTTAATAGCTGGTTTTACACCTTGATTTCGAGGTGAAA
WI-9274	25 CT	G		AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAGTTCTTAAAT TGTTTTGCAGTCTTTATGTTTATATCATAGGTATAGGTGAGCCTAAATCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACAGTTTTTTGTTTATGTTTTTAAGTAACTTATTATCTCTGGATTTCATG AAGGTGAATATCGTTTTTTTAACTGAATAGATTGTATAGCGATGA
WI-7313e	266 TC			AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAGTTCTTAAAT TGTTTTGCAGTCTTTATGTTTATATCATAGGTATAGGTGAGCCTAAATCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACAGTTTTTTGTTTATGTTTTTAAGTAACTTATTATCTCTGGATTTCATG AAGGTGAATATCGTTTTTTTAACTGAATAGATTGTATAGCGATGA
WI-7313c	256 CT			AAGGTGAATATCGTTTTTTTAACTGAATAGATTGTATAGCGATGA

WI-9281	68 G A ---	GCTAACACCTT TTAAACCGT	---	CAITTTATTTG AAAGCTATTCA GACA	ACTGGTGGGAGACTGTGAGGATCCAGGATTGAGTATTCCTGGCCAGAGGGCTTGGCTGGCTACTGG [G/A]GTGTTAGTTGAGTCTGTGTGCTTCCCTCTCTATGACTGTGTCCC
WI-7848	142 A G CTC	GTATATTACA ATGATCACOG	---	CCCCACAGAAC TATTGTAAAAC AA	TTCTGAAAATAAACCAGCCATTGAGCTATTTAAACTTGTAAATTTTTTAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAAATAAACATTAAATGCTAACACATTTTTTAA ACCGTCTC[A/G]TGCTGAATAGCTTTCAAAATAAATGTGAAATGGT
WI-9304	70 G A ACTGA	---	---	CCCCACAGAAC TATTGTAAAAC AA	TCACGTTTGGTGCTTCTCAGATTCTGAGGAAATTGCTTTGTATTGTATATTACAATGATCACCAGCT GA[G/A]AATATTGTTTACAATAGTTCTGTGGGCTGTTTTTTTGT
WI-7933b	314 C A ---	---	---	---	TTACAGAAACTTGGCCCTGTGCTGTGTCCCATGCTAGGGGCGGAGGGTCTTTTCCTTCTTTTCC TACCTACCCCTTTTCTTGGCCAGGGGCTCGTATCTTACCTTTCTTGTCCCTGGGCTGGCTGCAC AGAGATTGCCCTTCTCTTTTCAGAGCTGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCAAA AGTCTAAGGGACCATTGGCTGCCCTTGGGGAGGAACCATAGCTCCCT
WI-7933	96 G C ---	---	---	---	TTACAGAAACTTGGCCCTGTGCTGTGTCCCATGCTAGGGGCGGAGGGTCTTTTCCTTCTTTTCC TACCTACCCCTTTTCTTGGCCAGGGG[C/C]CTCTGTATCTTACCTTTCTTGTCCCTGGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCA CAAAGTCTAAGGGACCATTGGCTGCCCTTGGGGAGGAACCATAGCT
WI-7374	182 T A ---	---	---	---	CCCAGATGTGCCCATCACGTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTCCACTAACTGAAA CCATGGTGAGAAAGTTTGACTTTGTTAAATATTTGAAATGTAAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTCTAGCTGCTGTTGAAGAATATATTG[T/A]CAGAAACACAAAGGCTT GAT
WI-9343	78 C T CCTCTGCCA	CCAACAACAT CCTCTGCCA	---	AAATGAAACTT ACGTTTTTGTG TG	GGTCTGCTCTGTACCTTGACCCCTTCCCTTCTCTGCTTCTCTCTCATCATCATCCCAACAACAT CCTCTGCCA[C/T]ACACAAACAAACGTAAGTTTCATTTGGGCAAA
WI-7386b	104 T A ---	---	---	---	CTATATGTGAGAGGGGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAAATGTAAACAATTGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75 A G ---	CTTTAGAAAA TCTGCTTTAAC TTGG	---	---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAACCTGAAGAGTTCACTTTTGTATTAT GCTCTTA[A/G]TGATTACAGACTGATGCCAGACAAACCTTGGGAAGA
WI-9360	79 T C TTGG	---	---	CTTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGGGCATCTGTGTTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAATCTG CTTTAACTTGG[T/C]ATTCCTCTAATTGTGTTCCCTAGGAAATGACTGTCCCAAG
WI-7423	107 T C GTTC	TGCTGGGCTGT	---	GGTCCAGAAGA GGOOG	TGCTCCCTGTCCCATCTGCAGTGGACCCAGGACCCCCCTTTGAGGAGGTGGGGTGAACCTGCTCCTT GGCAGGGATTGTGACACTGCATTGCTGGCTGTGTTCT[C/C]GGGCTCTTCTGACCTTGCACCGTG GATACCAGGCCATGTGCCATGGTATTGGGCTCTGGGAGGTGGTGAATAAAGGCATAGTCT

WI-7424	131 T	CAAGAGAGAG AGAGGAAAGA A AAA	TGCAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGAGAGAGAGAGTTAGAGAAAAAGCCACCGAGGAAAGG AAAAACATCGGCCAACCTAGAAACGTTTTTCATTGTCATCCAGAGAGAGAGAGGAAAGAAAAA [T/A]ACAACCTTCATCTCTTTTGACGTTTCATAAACATTCACATA
X86400	118 A C	---	---	TCCTGCAAGAAGTTCTCAAGCCTTTTGATTTTGTGCAATAAAGTACAGCTTTGCATAAGAGTGAAA TTGGGCTAGCTTAATGGATCCATAAACCTTCTCTAATTTAAGTGAGAC/C]CTCTTTAAACACCT GTTAAATTAATGTAGCAGTCTGAGAACTAATAATATGTACCACCTCGTTTATTTGTTCAATCATCCA TCCCTTTCCCATGAATATTTCA
WI-8053	242 T A	---	---	GTGGCCACTACATGTTATAGAAACCATCATCTTGTCCACAGCAGCTATGAATAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCATTAAAGGTGCCATTAAAGGGACTTTTATCAACCTAA TAAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCAATTTTATACATGCTGAAAAGGGTCACA ATTAATCTTTGATCTTTTACTCACTGTTAACTTATATAAT/A]TTTCAAGAAC
WI-6190	165 G A	---	---	TACACAATGAATTGCTTTATTTTCGGTATGCATCCACATTTAGCATTTAGTGGTCTGAAACAGCAAG TGGAAGACGCGAGCAATTTGCCAGGAGGTCAAGCCACCAATTTTCGGGGATCTGCTGTGCACACCGG GTTCTTCTTAATCCCTGCTGAGGATCTTG[A]GAAGCAGCAGCAGCACCACCAAGGCATGCA CCGGATTCAAGGTTCTTTTGTCCAGTTGTCAGATTCCAACTAGACCCCA
WI-6275	148 G C	---	---	AACAGTCACCACCAACACATGACAACCTGCCAGGAGGCTTCTCCCTCCCTCTTTCGGTCCC ATGTGCTTAGTCAGCAAGGTGCGGAGGAGCACCAGTGTAGCTTGGCCCAAGGGAGTATTACAGAGA GAGGCTTGGGAAA[G/C]GGAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTCAGTAACGTGATGCTGAA
WI-6421	41 G T	---	---	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGATTG/G]GGGCTTCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTAOCCTGAGAGGGGATGGGGGCTCTCTCACAAA GAATATTTGGGGCAGAACCTTGGAACCTGGCCACAGGACATCCCAATATCCCTCTCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215 T A	---	---	GGGTGAGACGGGTTTATTTGTGCACATTTACAGCGTCCAGCGTCTGGGCTGCCAGCGGCATGCTC CTGTGGTGGGCTGCTCTACAGGGCGTTCACTTTTCTCACACACTATGTACAGTCAAGTGTCTCCAA GGTGATGGGCTACAGTGTGCTGATCAGTGAGTGTGTACACACATTTTACATAAATTACACAGGACTC ATACATGAAGAAAAT/A]AGAGCCTAAGGGCCTGTATTTTATGAGAAAAAAA
WI-9420	202 G A	---	---	AACTGTTTACAAAATAGGCTTTGCAAACTTCACTAGTAATGTAAGTCAATGACTGTGTTGTTT TAAATATGTACCAAGGAAATACAAATTGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACGTGCACAGGTGCAAGGAAACCGGAAACCCATTGTGTACACTGTCTTCACACAG [G/A]GCATTTCTTCTCACCTTAACTGCAGCTGTGCAAGATGCCTCAGTGTG

WI-9448	184	G A ---	---	TGGGGCTGCTTTAGACTTCATTTCTAGAGCAGACACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGGCTTGTTCCAAAGCTGAGAGCTGGCACAC[G/A]CACTGGTTTCTAAA TCTCTGGCTTGATTTATCCAAGCGCATGTTCTAACTGCGCGTGAGCAG
WI-9470	204	G A ---	---	ATGTCAGAAGAGACACAGACAAGGAGTTTTCCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAAGTACAGCTCTCCAGGTTGATAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGGAATATGATCTCCCTAAAGCCAGATTCTACTAGAGCCGCTGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCTCAAGCTCACAGGGCTCACCTTCCCAAG
WI-1245b	201	G T ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCTAGGGCAATGGTAGGTGCTGATGAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCTAGGGCAATGGTAGGTGCTGATGAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGT GGTTTATTAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A ---	---	TTCAGTGATAAGGACAGGTCTAGAACAGCGTTCCCAACCTGGCACCAATGACAGTTTGGACCAAA TAACCTTTGTTTCAGGGGACTGTCTACACATTTGGGATGTTTAGCAGCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCCAACATCATGACAAATGAAATGTCCTTAGACATT GCCAAATATACCTTGTGGACAAAATGGCCCTGATTGAGAACCACTGGTT
WI-5385	110	G A ---	---	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTGAAGAGG GAAGTCGATAATTTAACATAATGGTTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCTTTATCAACAGACTCTTTGAATCAATTTAGAGATCTCAGTGACCCCATGGCTAGAGTTCCTGAC CCCTGCTACGGGAACATTGAATGCA
WI-5403	199	T G ---	---	ACCAAACCGTTGGCAAGGCTCCCCAAGACTCACCAACCTTTGGTGCTTACCCATGCCGGGTG GGATTGAAGAAATAACCATAAATAAATTTGCTACAAATTTTCCAGTAGTTACCAGGCCAGCCCTAT TGGAAGAAATCATAAATGTAACTACAAATGTTATGCTCTCTGCTGGTGGCCAGGCATAGAGTT/G TGGCTACAACCCATTTATCATTGAACCTCAGAAGCATCCAGTTGGGCT
WI-5801b	157	G A ---	---	TGGTATTTTCTCTTTTCTAAAATGTTATGATTAATTAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAAATAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]JAGGGAATGAGAAAAGCACCAACAGAAAAAAGTGTGT GGCTTAAGGGAAGCCCAAGGAAGTTAAGT

WI-5801a	48	A G ---	---	TGGTATTTTCCCTTTCCTAAATGTTATGATTAATTAGTGTCTTTGTGAGAAATTTGAAAAAATGT AAATCAGAGAACAGAGAAAGAAAATAAGTATAGTTGAAACCTCTAACAAATTTAGATTTTAAAGGCC TAGGGAAGAAGAAAGAGAGCCTGGGAAGAGGGAATGAGAAAGCACAACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAAGTTAAGT
WI-5896	61	C A ---	---	TTCTATTTAAATCCTGTGCCCCATTGCAAGACTGCATTCAGTCTGCATGAGCCTTAGTTTC[C]AATAA AAGCCCTCAGACCGAGGACAATGTTTCAAGAACTAAATGACTGCAGGTGAGCAATCTCTGTATTA TACAACTGGACCAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGAOC TTATAATAGATTATAAGGCTGTGGTGAGTTTATTTAACTT
WI-7461	153	C T ---	---	TATTACTAGGTTTCATAGAGCCCCGTTGTATGATAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCTAACGCTCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGGAGCTGTGTCTC[T]GTTCCCTGTTGGGTCCCGGAACCCAGTGTGGTGGCTGGCACAGAG GAGCCCTGAGTAGCATGTGCTGCA
WI-9716	221	G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAAGTCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCTTTGGTATACCTTTCTCTTCTGAAGACCAAGCCTTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTTCAGATGTGTACTTCTACATCTGGAAGAACTAGATGAGTTAGGCTCTCTTCATCT CAATTGAAAATTTCTAGAA[G]A/AAAACACCTAAATTGGCTCATCTTGGATCA
WI-9760	49	C T ---	---	TTTTCGTTAAGTCTTGTAAGCCACACAGAGATGATCTACTCTCTTAC[C]TAAAGTGTACTTTGCA TATATTTATGGGGATGATCTATCCCTACTTAAGATTTTCTCTCTCAGGTAAATATTCATTTCTCT TTGTTGAGGAGTTCTTATTTGGCCTTCTTCTAAACCCCTAACCATCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31	A C ---	---	GAAAACCTCGTTGGCTCAAAGGAACTGTAG[C]A/AAATTTCTTTTATTTTGTTTTAACTC AAAGAGTGGAGTTTGCATTGACCTTGATGGCAGCTGCTCTTTTGTGTTGTTAAATCCTCTAGT GGGCATTTGCAAAAGCAATTTAGAGCAAGGTGGTGGCATGGAGTTGTGTGAGGTGCTGAAAAG TAGCAAATGGAAGAAAGGTTAATGGA
WI-10312	41	A G ---	---	AAGGCCAGTGGGAAAAGCAGACAAACACTCQAAGAATAC[C]A/GAGATAATAAACATCATCA GTAGAGATGGGATGACCTAGGAGGTGATGCTGATGAGGGCATGTGAGACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGAGTCTTCCAGTCCCATAGTAGGTGTTCCATAATAAAC AGTGACTAACTAGGTAGAGTCACAGAAGAAATTTCA
WI-11152	179	C T ---	---	GATCTTTGGACATGCAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAACGAGCCCTA ATTATAGAACAGACTCTACAAAGGACCAGTTAAAGGTCTCGCACCCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAGTGGGACAAAAGGCTTGTCA[C]TCTGTCTCAGAAACATTTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167 A G ---				TGGTGAGGAGCTGTAAAGGCTGAAAGAATAGTCTCTGCTGCTGTTGGTGGAAATGGATGAGTCTCT TTTACAAAATTTTCTCTGGCATGGGTGTATGTTTGAATCATGGAGTTGGAAGACTTAGATTCA ATTTGGGCTGTACAGTTTACTGGAAGTTGTA/GTGAAGTCTGAGCAAGTGTCTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198 G A ---				GGGTTCAATTAACAGCCTTCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGGCCACTATTGACTTGATAACACCTACAAAACAACACATTAAACTCTCCCACTCTA CCCGCAAAGTCTACCTTTGGTCTTTTATTTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164 C A ---				TTTATCTTCCAAAACCATGTGTGTTTCTTCACATACATTAGTAAATTTAAATCATGTCATTTAATTA TGCACCTACTTGTGGCTACAGACATTGCTTCCAAATGTAAATTCCTTAACAACAGCAAGCATAACT GATGTCCATCTTTGATTTCTCTAAAA[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGT CTTCTCTGTTTCACCTCTGATTTCCCTATTTCAGCATTCATGATTA
WI-4860	72 A G ---				AAAAAACAACTTCATTTGACATTCTAAGAAGATAAAGAAAACAACGATCCACTGTGTGTTTGCTT GATTTA/GJGGAGATAAAACCTGATCTCTAAGAAAATTAACCAAAGCAGTACACTAAAAATAGCCT TTGTGTGTGTTTTTCAGGAAAGAAAGCCAAATCCAACTAAGTTGCTAAGAAAAATAATGTTTCATATCA CTCTAACTTCCACATAGAGCATTAAATATAGCA
WI-9705	111 C A ---				TGAAAGGACCAGTTCGAATGCCTACCAAGGTAAAGTAAATCGGAGGGGCAGGAAGTAGAGGTTGCTT CCGGATGTTGCATAAAATTCAGGTTCTTTAAGGAGTTCGGCTGCC[C/A]AAAAATTTGTTAACACTGATGC TGCTACAAACGCACATAGAAATCGGTGGTAGATTGCGGTTCCCTAGTAAGTAGCTAATGTTTAGATA TGATTGTTGAATTATTGTTGCTGTGTTCTTGGTG
TIGR- A004Z48	177 A G ---				CAATAATCTCTGCTTAGAAGTTGCTTAGGGCCATGGATTGATTAAGGTGGGCGCAGGTGGAGCTG AAGATCTGTTGGCAGGCTCACAGAGACGGGGTGAGGGAGAGATCGTGGTTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGA/GJTCCTCCAATTTACAGGGCTCCC GTGGGATGTTGGAGGCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34 T G ---				GGGATTCAATGTGTCTGCTCATCCAATAAGCACT/GJCATGACCTCAGCCCCATACTCTTCTTCCC TATGTTCCAGAGACAGAATAGACCTGGCCCCCTTCTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGGAGAGGGATCCTTCTAGTTGA
WI-7747b	88 T G ---				GTGAGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTTTAATTTGATT/GJAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTGTAAAGTT ATTCTGTGTTGTTGTTGGGTATCCTGCCAGTGTTGTTGTTGTTAAATAAGAGATTTGGAGCACCTGTA GTTTACCATTGTAATAAAGTATATAATTTTTTATGTTTGTGTTCTGA

WI-7747a	44 T C ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTCTTTCTGGCCTGCTCJTTCGTTAACTGTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACACGCTTCATGCCCTTTGTAAGTT ATTCTTGTGTTGTTGTTGGTATCCTGCCAGTGTTGTTTGTAAATAAGAGATTTGGAGCACTCTGA GTTTACCATTGTGTAATAAGTATATAATTTTATGTTTGTGTTCTGA
WI-7189	197 T C ---	---	TCAGAAATTTCTCTTCAGCTCATTTTGCTCTCTCACAAATTAAGGAGTAGGTTAAGTGAAGGT CACATACCATTATTTCCCTTCAAAACAATAATTTTACAGAAGCAGGAGCAAAATATATGCGCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATATTAAGCCTACAACAATTTTTC/JAG TTTGCAATAGAACTAATACTGGTGAAATTTACCTAAAACCTTGGTTATT
WI-7850	57 G A ---	---	AGCCCCAGCTGGACTATGGATGTGCACCTTTGCTCCCTGCTCTTTCTGCCCTGGG(JA)CTCATGTA TCTGCGCAGCTCTGTACCTCTGTGGTGCCATCTCTACCTCTGACACAGACTGCCCTTGAAGCT GAGAAGCACAGGGCAAGGAGCAAGGACCACAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAATCAGGGGGCTGCTACTAGAGCC
WI-7907	69 G C ---	---	CTCTCTCTTCATCCCATCACCCCTAAATAGGTCAGGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G(JC)JAGAAAGTGAAGGAAGATAGGAAGGATATTACCTCTTCTGTTATTTTAAAGAAACATTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTTAGAGGCTAAATTTATCTATAAATATATATAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAATATTGTCAAAGTTTAAAT
WI-7919	242 T C ---	---	GAAGGCAGCTGGATCACTCCCGCAGTCTTTGGGCAGCGCTTGTGTGGAACACGAGAGCTCCTCCT CAGGGGCTGGCAGCTCACCTCTATTCTGTATGATGTTATTTGGTTAAACACTGTCAAAATAATAGAGAT GTGCCAGATTTAGATTTCTTACCCTAATCTGTTTAAATATGTAACCTTATTCCTTTGAAAGTGTC AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAA(TC)JACAACTTT
WI-7928	101 T G ---	---	CTCCCTTCCTATGTCTCTCAGCAGCAGCTTGGGGCAGCACTTGTTCTCTGACCGTTTGTGGGCTA TTCCCTTCGAGTGCAGACATCGTCAAAATTCAT(TC)JACAAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGGCACTTTAAACTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCATTAAAAATACGTACATTTTCGAGGTAATGGTA
WI-7936	131 T A ---	---	TTTTGAGTCAAGACTTAAAGGGCCCAATGAATTTATATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATTCCTTTGGAGTTAAATGACATATAGACATACACCCAAACACTTACACCAAC(TA) ACTGAATGAAGAAAGTATTTGGTAACCCAGGCCATTTTGGTGGGAATCCAAAGATTGCTCCCCATATG CAGAAATAGACAAAAGTATATTAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99 T C ---	---	TACACGTTCCAGCCGTTGCCACTCATCTGCGGCTTGTCTTTGGTGGGGGCGAGATTGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTCATG(TC)JAGCCCAAGTACAGCCTGGACCACCCCTGGTGTG TGAGCTAGTAAGATTACCTGAGCTGCAGCTGAGCCTGAGCCATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGCCATTGAACTAAGAGGCTCTCAAGTCA

WI-7805	101 A G ---			TTTCTAGGCTGACAGTCTGATGCATGATTTTTTATAAATATTTTCATACTCTGTGAAATTTGGATCTT TTTACTTTGAGCATATATTTAGAATATGTGTAGTGTAAAGGATCTCCACAATGTGTCAGTGTG AAGGCAGGTTTCATTTGGAAATAGTTTAAACAGTCAGGAAGGCTAAACTGGTCAGTATTAATGTGTAGC CCTACCAAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---			GGCCAGGAGATTAGCAACAAGGATTCATTCTGTTACTTACTTGCOCCTTTTATCTTCCCTCTTGCCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTCTTGCCAGTGCT [G/T]CTACTCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACAACACTCAAAATGGCAATGTCATCAG
WI-140	252 C T ---			ATTTGAAGATTGGAGGGCTTGCAGAGGAAAAATAGATTTCAATTGGATCCCAAACTATAATGACA AGTTTTTAATTAGGTGATCAAGGCTTCTAAAGTGAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCCATTACGCCAGCTCATTTGCCAGAAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAAATTTAGTTAAAAATGTGTCAATTTGTCTGTATTGGCAATCCCTC/
WI-198	218 C T ---			GAGGTCTTCAGCAACATGGAAGCCCTACTGCTTCAACCCGAGTTCCCGGATCAAGTGTGGCAOC CATGATGAAAACTCTGCCATGGTTTAGTACCCCTGGACCAAGTAGTCAATCCCTGACTTTAAAA TTCTAAACAGCCTTGTGATGGACAATCTCTGCTAAAGACTAACCACTTCCCTTATCTTATCTTCAGCTA CCTGCTTCCCTTTC[CT]GTTTAAACAAAGCATAGATAATCTGAACAAC
WI-205c	146 T C ---			TTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAAAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTGT[C]CCAAAGGCTTGATGGGAAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTATTTTGTGTTAGTTCCC
WI-205b	146 T C ---			TTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAAAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTTGT[C]CCAAAGGCTTGATGGGAAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCCTTATTTTGTGTTAGTTCCC
WI-234	165 G C ---			GAAGACTGAGTTTCCAGGAGTTGACGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCACCCCAAGTCTTCCAGAGGCTCAGACTACCTCCTCCATCTCCCCCT CTCCCCCAACACACAAATACAGAGATT[G/C]AATTCAGGAGCCAGTTTCTAGGTGGGCTTGAGC AATCATACACAGTAACTCTTGGTGCTTATGTTTCTCAATGGGAAATGG
WI-276b	25 A G ---			AGCTTTTGAAATCCAAAACCACAT[AG]CTTGACTCTCTTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAGAAAAATACAGAACACCCCTGTGGCTGCTGACGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAAAGCATCTCTCTGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTTATCCTCTGCTGCTATCCCTGATCCCTGATGCTGGGCAA

WI-276	25 A G ---	---	AGCTTTTGAATCCAAAACCACATAGCTTGACTCTCTTATCTCTCTCTTGTGTAACATCTATCC CTGAGGCAGAAAATACAGAACCCCTGTGCTGCTGAAACGAGGAGGATGGGGCGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGCTTATCTCTCTCTGCTATCCCTGATGACTGGGCAAA
WI-427	59 GA ---	---	TTTCCCAATCCACAGGTAACAACTAATAATGATGTATAGAAATTTAGAAGTCTCCGAGTGT TTCCCTGGGAAAATATTCACAAAACATTTGTGCTGCTGCAATCAGGTTAAAGACATAGTGTGCCA TTGTGTCATCAGACAGGTAGAGGCTGACTCTGCGAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCAATTTATGAGCCAGGGTCTGCTCTGTCACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCACAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA/TTC/JAAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAAACCAATAATCTCTCAGGTAATTTATGCCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCACAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA/TTC/JAAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAAACCAATAATCTCTCAGGTAATTTATGCCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCACAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTT/JC/JAATAAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAAACCAATAATCTCTCAGGTAATTTATGCCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	GTGTAATTTGGTGGCTTTGCACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAAGTATCCTTAGGATATTCT GATACATG/JG/JTAATGACCCCTCCATGACTCTGGTACCTCATCAATACCAATGTGAGAAATTAAAC TTGATCTAATAATTTCTTCACAACCTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141 A G ---	---	GTGTAATTTGGTGGCTTTGCACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAAGTATCCTTAGGATATTCT GATACATG/JG/JTAATGACCCCTCCATGACTCTGGTACCTCATCAATACCAATGTGAGAAATTAAAC TTGATCTAATAATTTCTTCACAACCTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136 A G ---	---	GTGTAATTTGGTGGCTTTGCACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAAGTATCCTTAGGATATTCT GAT/JG/JCATGATAATGACCCCTCCATGACTCTGGTACCTCATCAATACCAATGTGAGAAATTAAAC TTGATCTAATAATTTCTTCACAACCTAATAATACCTGAGAGAAATAAGTCTATTTAAT

WI-611	66 G C ---			TTCAAATTTACACCAATTGGGTATATTATAATTTNGCTCTATCCATAGTTCTAACCCCTCTCTCTTG/ CJACAGTGAGACACCTGCCTTCTATTGTCTTGACGTATTACGTATTTCGATCAGTCACCCATCTGGA ACCAAGGTTTCATTTCTGTGACCCCTCCCTCCTCACCCCTACTTGGGCTCTGACTCTCTTTCCTGGGCT GAACCTTCTCTGTGGCTGTCCGCTTCTCTGCTTGGGCTCCAATAC
WI-681b	156 A G ---			TGAAGCCCTCTCTCTATACCAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTCATACAGGGGAAGCACCTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
WI-681	156 A G ---			TGAAGCCCTCTCTCTATACCAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTCATACAGGGGAAGCACCTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
WI-867b	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAAGGCTCCAGTATCTGGCACATCTTCCCTTTTCATCTCCG/GAJTTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGTC AGTGCATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAAACTTA
WI-867	113 A G ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAAGGCTCCAGTATCTGGCACATCTTCCCTTTTCATCTCCG/GAJTTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGTC AGTGCATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAAACTTA
WI-867	119 G A ---			TCATCAGACCTGAGATTGAGATGAAATCTACCAAGGTACCACAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAGAGACCCACCTACCTCATG/C/GJAAGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTGTAAATGCACCTGTTATGGCCTGAAATGTTGTACCC TAAATTCTATATGTTGAAGCCCTAACACCCCAATATGCTGTATTGTACATAA
WI-871b	123 C G ---			TCATCAGACCTGAGATTGAGATGAAATCTACCAAGGTACCACAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAGAGACCCACCTACCTCATG/C/GJAAGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTGTAAATGCACCTGTTATGGCCTGAAATGTTGTACCC TAAATTCTATATGTTGAAGCCCTAACACCCCAATATGCTGTATTGTACATAA
WI-871	123 C G ---			TCATCAGACCTGAGATTGAGATGAAATCTACCAAGGTACCACAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAGAGACCCACCTACCTCATG/C/GJAAGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTGTAAATGCACCTGTTATGGCCTGAAATGTTGTACCC TAAATTCTATATGTTGAAGCCCTAACACCCCAATATGCTGTATTGTACATAA

WI-884	198 T C ---	---	AGGTTCTGGACTTGATGCTGGGAACAATTGGGTCCTGGGAAATTCCTATTTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCTGATCTATTGGGA ACTTCTCCTAATAGATCAGGAAATCCACCTCATTAAATCATGACAAACNNAAAAGGAATAT/CJG ATCCCGCATGCAACATTTATTCAGTGAAACATGATGAAATGAACATAAT
WI-921b	205 G A ---	---	CACCTCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACAGGGACAGTTTACTGG CAGTGATGCCTCTCACGCTGCCCCCAAGAAAGTCTTNGCCAGGAAAGACCGATCCATCTAC TCTG/AJGGGAGAGATCTGACAAATTAATCAGGAGGAAGAAATCTTCCGAG
WI-921	205 G A ---	---	CACCTCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACAGGGACAGTTTACTGG CAGTGATGCCTCTCACGCTGCCCCCAAGAAAGTCTTNGCCAGGAAAGACCGATCCATCTAC TCTG/AJGGGAGAGATCTGACAAATTAATCAGGAGGAAGAAATCTTCCGAG
WI-945c	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAGNA GAAAGAGACAGNGATTGGCTAAC/GC/CATGCGAGTAGTGGGCCCAAGGCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAACANTAGGTGCAGCACANNNGGTT TTCTCTGTGATAGATCTCTTAAAGGGAATCATGACAGATTTTCTGGCTTTA
WI-945b	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAGNA GAAAGAGACAGNGATTGGCTAAC/GC/CATGCGAGTAGTGGGCCCAAGGCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAACANTAGGTGCAGCACANNNGGTT TTCTCTGTGATAGATCTCTTAAAGGGAATCATGACAGATTTTCTGGCTTTA
WI-960b	167 C T ---	---	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTGAGCAACCTAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTACCC CTGAGGAATTTATCAAAGATGTTAAGTTATCT/CJCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 G A ---	---	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTGAGCAACCTAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTACCC CTGAGGAATTTATCAAAGATG/AJTTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 T C ---	---	TCCACTGAGTATGGCTTTCAGTAGTTTTATTATGATGTCCTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGTTACTTTGGGAGAAATGCTCACTATAAATATTGCTTCTGACCCCTTTCTGTGTTG CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTAT/CJGCTGTTTTTACTCTCCTCTG ATTTTTTTCCATTATTTTATTGCTCTGGCTTCAATTTTGTAATNTG

WI-1147b	204	G A	---	---	TTGCCATTATTGAAGATAACCCACACCTTGGTGTCAGGGTTTCACAGGATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGCCACCCGCAACTTCCTCTCCCTGCTGGCTC CTGAGCCAAAAACAGGCATTACCATAAATCACTTTGTTAGGATGAACCTATCTGGCCAAACTGATA C[G]A[GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147	C T	---	---	GCATTGAGAGGGTTCGTTAATGACATTCACTGAGGCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAATACAAATGATGTCCTGTCCTGAGTGTCTGAATGCGCCAGGTGGC TAAGTCTGGGG[C/T]CTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124	C G	---	---	GCATTGAGAGGGTTCGTTAATGACATTCACTGAGGCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAATACAAATGATGTCCTGTCCTGAGTGTCTGAATG[C/G]GCCAGGT GGCTAAGTGTCTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124	T C	---	---	AAGTTACAGAAAAAATACCAGAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTCAANGTNCACAGACACTTATCCCTAGACAGCCATTCTTTTGAATG[C/G]GNCANT AAAAATGATTGAAATTGGGAATAAGCCCTCCCTCTAATGATTGACAGGTGACACCTTGCTTAG GCC
WI-1305d	202	C T	---	---	TTCTCAATCCAACTGTGTGTTACTTTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46	C T	---	---	TTCTCAATCCAACTGTGTGTTACTTTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATGATTGTGCAAAAGTATTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153	T C	---	---	TTCTCAATCCAACTGTGTGTTACTTTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202	C T	---	---	TTCTCAATCCAACTGTGTGTTACTTTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248 A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCGGTGTCATTTAGAAGCCATAGAGATAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAACTCTGAAGCTGTGACCTAAGGNGAGAGTGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCTCTA/GIGC
WI-1306	240 A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCGGTGTCATTTAGAAGCCATAGAGATAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAACTCTGAAGCTGTGACCTAAGGNGAGAGTGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTA/GITCTTCTTAGC
WI-1307b	118 T C ---	---	GACAAGGCTGGTACTAGTTTCCAAATCCAAATCTATGTACACTTCTCTCCTCCTCAAGTGGACA GATTTCTGCATTACTGCTGGGTGGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGCTTT CCTACCCCTTAAATGTATCTTNTCTAATTATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGGTGTTGTTGTGTGCTGTGTTTCTCTCTGTAAAGNTGTTT
WI-1307	118 T C ---	---	GACAAGGCTGGTACTAGTTTCCAAATCCAAATCTATGTACACTTCTCTCCTCCTCAAGTGGACA GATTTCTGCATTACTGCTGGGTGGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGCTTT CCTACCCCTTAAATGTATCTTNTCTAATTATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGGTGTTGTTGTGTGCTGTGTTTCTCTCTGTAAAGNTGTTT
WI-1325b	169 T C ---	---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165 C T ---	---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162 T C ---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAGAGTCTGTATTGTATAA ACACCAAGTGGCGTTTAAATGGAATGCGTATGTGTGAGTNCATATTACGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTCJ/GAAGTTGGGTAGTACCAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTCCATCTCTAAG
WI-1327	175 C G ---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAGAGTCTGTATTGTATAA ACACCAAGTGGCGTTTAAATGGAATGCGTATGTGTGAGTNCATATTACGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTAAGTTGGGTAGTACCAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTCCATCTCTAAG

WI-1341b	136	G A ---	---	TATCAGCATGATTGTGGCTGTTGGACACAAAGTCAATTGTACTTTTGTGNNNTCCTTTTCNTTT ACCTGATCCACTATCTTCTCAAGATCANGTTCAAATTTGGCTTNCCTTTGTTNAATTATACCCAAAGC IG/AIGGATTGTGATGGATCTGTTTATTTCTGTGCTTGGAAACGACAGAGCTCTCTGNGAGTNTG GTTTCAGGATTGTCTGTCTCTGTTCCCCAGCCCACTTGCACTTAGCAAGTGT
WI-1349e	192	G C ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCGAGGCGAGGTGGTAGGTGCTGGCCTGCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTGTGAATTTCCATCTCTGAIGC/JTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATA
WI-1349d	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCGAGGCGAGGTGGTAGGTGCTGGCCTGCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTGTGAATTTCCATCTCTGAIGC/JTCAAA ATTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATATGAT
WI-1349c	192	G C ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCGAGGCGAGGTGGTAGGTGCTGGCCTGCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTGTGAATTTCCATCTCTGAIGC/JTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATA
WI-1349b	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCGAGGCGAGGTGGTAGGTGCTGGCCTGCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTGTGAATTTCCATCTCTGAIGC/JTCAAA ATTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATATGAT
WI-1349	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAAATCAGTTAGTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCGAGGCGAGGTGGTAGGTGCTGGCCTGCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTGAGTGAAGGATAGTGTGAATTTCCATCTCTGAIGC/JTCAAA ATTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAATATGAT
WI-1403b	57	C T ---	---	TGGTATTGGAATGGGTTTCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAGTTGCT/JTCCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAATATACGT AAAGTTACATCAACATAATTCTTGGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTCA TAATCCCAAGTGCCAAAAGGGTTGTATCTGATTTGT
WI-1403	58	T C ---	---	TGGTATTGGAATGGGTTTCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAGTTGCT/JTCCGA TGCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAATATACG TAAAGTTACATCAACATAATTCTTGGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTC ATAATCCCAAGTGCCAAAAGGGTTGTATCTGATTTGT

WI-1417c	31 C T ---	---	---	CAGGCCGAAGAGATTACGTGAGAGAGATGTC/TJTTGGCCAGGGGGGCGAGATGTGAGCCCCACGGG GGTGACAGCATGCTGCTGGCATTTGAGGGGCCCCAGAAAGAAATCCAGTGGCCCTCTCAATGACTTG GGTCTCTCGACTTCGGAAGTTAAGGGGCTCGCTTCAAAAAGCTGGGTCCGGTTTGAGCGGGTTGC AGCGGAGGCCCTTAGGTCCGTATTTAATGTTTGTCTTGTAGAAAAAGTGGC
WI-1417b	31 C T ---	---	---	CAGGCCGAAGAGATTACGTGAGAGAGATGTC/TJTTGGCCAGGGGGGCGAGATGTGAGCCCCACGGG GGTGACAGCATGCTGCTGGCATTTGAGGGGCCCCAGAAAGAAATCCAGTGGCCCTCTCAATGACTTG GGTCTCTCGACTTCGGAAGTTAAGGGGCTCGCTTCAAAAAGCTGGGTCCGGTTTGAGCGGGTTGC AGCGGAGGCCCTTAGGTCCGTATTTAATGTTTGTCTTGTAGAAAAAGTGGC
WI-1729	172 A ---	---	---	CCATGAGCAACAGCATGTTTCTACTCTGTGATGTGATGTTAGGGGGCATGTATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAAGA TGTTGGAGAACTGAAAAAGAGAGCTTACATGCACCCCAATAGCAAACTCTCCACACATTTCAGCA GATGATGTGTCTCTCCGTGGTACCTTCTCTCCACCACATCACTGTGTTTTT
WI-1732b	122 T C ---	---	---	TGCCTTACTTCTTGTTCATCCACCATTACATTTGTAAATGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGGAGTNTCCCTGGTCAACCTTT/CJATTACAGTCT CTGCCACATGTCTAGTAAGTGTGAGTGATGGTGATCAGTATATCTCGAGCCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1732	114 C T ---	---	---	TGCCTTACTTCTTGTTCATCCACCATTACATTTGTAAATGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGGAGTNTCCCTGGTCAACCTTTATTCAGTCT CTGCCACATGTCTAGTAAGTGTGAGTGATGGTGATCAGTATATCTCGAGCCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1750	97 A G ---	---	---	GGGAATTTAATGACTCCAAAGGTAGTAATTCCTTCCCCCAAAAAAGGTTTAAATCTGTGTGGA CATAATGTTTGAATTTGCAGTTCACTTGG/A/GJTTAAGGTGTGCTGTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAGGGCTAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCTGACTGAG CTACATTCACCTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---	---	GGTACACAAGAAATGCTTCTGGAAATCTAC/A/GJTAGCGCCTTAACATTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCAACCATGAAGCTGGCAAGAAACAATTCCTAGGAAAAGTACAATTAC TGGGAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAGAATAATCATAAAAAAT
WI-1803c	77 A G ---	---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCAGAA CCATTATGATAGJAGTAGGTAGGATCAGCATCAGCTGGGAGGACATATCTGGAGTNAGATATCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAAATTACTTATTACTCTTGTCTCAA GGAAATGGGAATACCTATAATACAGTCTATTGAGGAAAAATACTGGAATCA

WI-1803b	77 A G ---	---	CCACTCAGTAATAAGTGTGGAGATAAGTATATGTTAGGCACATAATAATATTTTCAGGCAGAA CCATTATGATAGAGTAGGTAGAGCATCACACTTGGGAGGACATATTCTGGAGTNAGATATCCTG GGTGCTAATTTCAATATATCTACTAAGCATGACTTCTAGAAAATTACTTATTACTCTTGTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA
WI-1837b	112 C T ---	---	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATACIC/TJCTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGAACTTTAGCTTTCTGCTGGCT
WI-1837	112 C T ---	---	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATACIC/TJCTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGAACTTTAGCTTTCTGCTGGCT
WI-1840b	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACCTG/TJGAGAACTCTGAATATTCAGCACATACAAGTGTGACAAACCACCTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACCTG/TJGAGAACTCTGAATATTCAGCACATACAAGTGTGACAAACCACCTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	GGGCTCACTTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTCTTTTCATAACTTACTCCCGG CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTTAC/TJGCTGCNAAATAAACTCCCAAAA AAGTGTTAGTCCACAGGGTTTAAATGTTCTTTGTAATGAATTTCTGTGCGACCCCTGTGCCTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T ---	---	GGGCTCACTTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTCTTTTCATAACTTACTCCCGG CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTTAC/TJGCTGCNAAATAAACTCCCAAAA AAGTGTTAGTCCACAGGGTTTAAATGTTCTTTGTAATGAATTTCTGTGCGACCCCTGTGCCTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T ---	---	TGTTCTCTGGTCCAGGCACCGGCTAAGTCTTGCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGGCTGCTCTGAGAGGT AAAGTGCCTGCCCAACCGGCACAACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAAGTCCCATGAGAAACCACCTTTCTTTGCTCC

WI-1900	119 C T ---			TGTTCTGTGTCAGGCAACGGGCTAAGTCTTGTCGATAATGGAATAATCAACTGGACAACCCOONG CTNAGGTAGGNTACCTNGGCAATTAGCCCATTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTCCCTGCCCAACGGCAACTAGAGAGCAGCAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTCTTAAGTCCCATGAGAAACCACTTTCTTGGCTCC
WI-1943c	165 C T ---			ATTCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCAITTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165 C T ---			ATTCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCAITTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164 C T ---			ATTCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCAITTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270 A T ---			CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGGAGTGAGGATCTCGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270 A T ---			CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGGAGTGAGGATCTCGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1977	203 T C ---			CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTCATAGAGTNTGTTTGTAGTCTCGTAATAACTGTGCCCTAGGAAGGTTGTT TTCTACTGCGTCTGTGAAAGCCTTTCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATTIT /C/TAAACATCAACACTGGCTGAGGCTGTGG
WI-2012	102 T C ---			AAATCTAGAAGCCAGAGTCAAGTCAAGTATATAAGTTGAAGTAATGCATTGTAGTTTCATGT TTCTCTTAATCTGCACAAAACACTAGTAAAAATC/T/CTTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGTGTCTCTGAGTCACTTTTTTCTACTCTCAT GGCTTACCAATGCTTCCACTGGATC

WI-2013	127 C T ---			CTTTAGAGGTGGTCATTTCCGGTCCCTTCTGGAAAGTGATTCCGTGTTTAAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACTGACACTC/TCTCA CCAGAAAAAGAGAAATACCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGGATATCTCAGCTTTCTGAGCCCTGGTTACTGCAATCC
WI-2032c	166 G A ---			ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAAC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAAC ACATCACCCAACTGGTTTCTAGATGTACAC[G/AJTGTTGGGACCTCTGTCTCAACCTCCGACTTTCAC AGATCATTGGTTAGGCTCACCTTCCCTGTAATTGCTTCTGTTTTTCAAGGG
WI-2032b	219 C G ---			ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAAC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAAC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA[G]CTTCTGTAATTGCTTCTGTTTTTCAAGGG
WI-2032	219 C G ---			ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAAC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAAC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA[G]CTTCTGTAATTGCTTCTGTTTTTCAAGGG
WI-2054b	188 C T ---			CGTTTCTTCTACATCTTGGGNACATAAAGANGAAGNAGCTGCTTTTGTGGTAGTTTGGCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTC/TJCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGCTTT
WI-2054	183 T C ---			CGTTTCTTCTACATCTTGGGNACATAAAGANGAAGNAGCTGCTTTTGTGGTAGTTTGGCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTC/GJTTCTCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGCTTT
WI-2573d	129 T C ---			TGGGATTAAACCCCTGTTTCTCTCCAGTTTCAGTGTGCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTGTTCCGTGCTTTC/JTGA TATCATCTGATCTTCCCAACAGGGCTTATTATGCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C ---			TGGGATTAAACCCCTGTTTCTCTCCAGTTTCAGTGTGCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTGTTCCGTGCTTTCGATAT CATCTGATCTTCCCAACAGGGCTTATTTC/JTGCCTAGGTAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG

WI-2573d	129 T C ---	---	TGGGATTAAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCGTTTCAAGGTGTTCCGTGCTTT/CJTGA TATCATCTGATCTCCCAACAGGGCTTATTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAAGGTATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C ---	---	TGGGATTAAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCGTTTCAAGGTGTTCCGTGCTTTTGATAT CATCTGATCTCCCAACAGGGCTTATTACJTGCCTAGGTAAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCACAAGGTATATGGCTGGGCTTGGACGAG
WI-2573b	165 A C ---	---	TGGGATTAAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCGTTTCAAGGTGTTCCGTGCTTTTGATAT CATCTGATCTCCCAACAGGGCTTATTACJTGCCTAGGTAAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCACAAGGTATATGGCTGGGCTTGGACGAG
WI-2573a	129 T C ---	---	TGGGATTAAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCGTTTCAAGGTGTTCCGTGCTTT/CJTGA TATCATCTGATCTCCCAACAGGGCTTATTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAAGGTATATGGCTGGGCTTGGACGAG
WI-2868b	60 A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAATTTACAGACATTAAGAACAAGCTTTCCJAGJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTAGGTCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAAGCTTTCCCAATGATGAGCCCAAGTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60 A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAATTTACAGACATTAAGAACAAGCTTTCCJAGJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTAGGTCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAAGCTTTCCCAATGATGAGCCCAAGTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131 T C ---	---	CATGCTGTGTAACCTCTGTGCTGCTGCTGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGAIT/CJ AGAAATGAATAGAGCCCAATTTAAATTATATACAGCTTTATGTCCACTTCTGTTCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT
WI-2870	131 T C ---	---	CATGCTGTGTAACCTCTGTGCTGCTGCTGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGAIT/CJ AGAAATGAATAGAGCCCAATTTAAATTATATACAGCTTTATGTCCACTTCTGTTCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT

WI-2954c	49	T A	---	TTAGCACATATCTGTTGGGACTTAACCTAGACAAAGGCATAAAAA/T/A/CAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAAITTCCTCATACCTACCCCTCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAGTCCA GAG
WI-2954b	41	A G	---	TTAGCACATATCTGTTGGGACTTAACCTAGACAAAGG/GJTAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAAITTCCTCATACCTACCCCTCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAGTCCA GAG
WI-2954a	38	G T	---	TTAGCACATATCTGTTGGGACTTAACCTAGACAA/GTJGCATAAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAAITTCCTCATACCTACCCCTCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAGTCCA GAG
WI-2971b	62	T C	---	ATTACAAATCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCAATAAGCTTCTTTCAAACAATTTGTAACTCTCTCTCTTAATAAACCTAAG ATTTCCTTTGTTCCCTGACATTCGAAAGGCCACGCTGTAGATGTATGTCCAGATTGCAATCCT AGTTCITTAATGTTATTCTGAAGAAACCTTTTACTTAGGGATTGTCT
WI-2971	62	T C	---	ATTACAAATCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCAATAAGCTTCTTTCAAACAATTTGTAACTCTCTCTCTTAATAAACCTAAG ATTTCCTTTGTTCCCTGACATTCGAAAGGCCACGCTGTAGATGTATGTCCAGATTGCAATCCT AGTTCITTAATGTTATTCTGAAGAAACCTTTTACTTAGGGATTGTCT
WI-2995d	133	A T	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGOC TCCAGTTTNTATCAAGATAAAGACCTGGAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTT/A /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCCACTGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151	G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGOC TCCAGTTTNTATCAAGATAAAGACCTGGAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTTNA AATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCCACTGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133	A T	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGOC TCCAGTTTNTATCAAGATAAAGACCTGGAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTT/A /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCCACTGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151	G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTNA AATCTTCTCTTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTNA /TAAATCTTCTTCTGGTGTTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151	G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTNA AATCTTCTTCTTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151	G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTNA AATCTTCTTCTTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133	A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTJA /TAAATCTTCTTCTGGTGTTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-3147	85	C T ---	---	ATTCTGTAATGTTTTCACTGCTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA T/CJGACAAGCAAGAAACAACAGAAAGCCCTGTGTGCAATCTGGCCCTTATAAATACCTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTATTTTNATATCTTAT
WI-3234b	68	T C ---	---	ATTCTGTAATGTTTTCACTGCTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA T/CJGACAAGCAAGAAACAACAGAAAGCCCTGTGTGCAATCTGGCCCTTATAAATACCTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTATTTTNATATCTTAT
WI-3234	68	T C ---	---	ATTCTGTAATGTTTTCACTGCTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA T/CJGACAAGCAAGAAACAACAGAAAGCCCTGTGTGCAATCTGGCCCTTATAAATACCTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTATTTTNATATCTTAT

WI-3292b	106	G A ---	---	---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTAGCTCTGCACCTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTGAGTGGATGGGATGGGATGACTT GCCATGAATATTTCCATTGTTCTCATTAAATGATTAATAAATAAGTAAATAATATTATTTNCCATGA GACACAATGGAAAAATGGAAAAACATTTCATGGAAAAAAACCCATTTCAAATC
WI-3292	106	G A ---	---	---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTAGCTCTGCACCTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTGAGTGGATGGGATGGGATGACTT GCCATGAATATTTCCATTGTTCTCATTAAATGATTAATAAATAAGTAAATAATATTATTTNCCATGA GACACAATGGAAAAATGGAAAAACATTTCATGGAAAAAAACCCATTTCAAATC
WI-3355	19	G C ---	---	---	---	CCATGAACCATGGGTACA/GJATATTCCTAACTTCAGAGTCCCTCTACTGGAGAGGGATCCCA CTTTTAAATATGATTTCTTGAAGTGGTGCATACATACTATTCCTCCCAAGCATTAAAACTCATCAGAA AAAAATCATCAAAAGTCGAAGTAGTTTNAATTAACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	G A ---	---	---	---	CCATGAAGAATGAGTTCCTCCCTCCCTGGGTACGCTGAAGAATAGCACACCCCTTGAGAAATTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCTCCGCTCTAAGACACACCTTTATGCTTTCNAAGCTTT CTGGAATGGGATGAATCTNACATTCAATGTGCACCCCTCGTGTGGATCAGTCTCTCCGAGTGGCCCC ATCTCTGGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAAATCAGG
WI-3505b	131	G A ---	---	---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTTCCTCCATTTGTGCATCAGTGCACCTTAAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAAGTCTCTAAGACATTAACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANANGAAAAAATGTTGATGATACCT GTTTAATTGGGAAATATGTTTGCATAT
WI-3505	131	G A ---	---	---	---	TAACCTATGCCTCATCTGGCTTACTGCTTAGTTCCTCCATTTGTGCATCAGTGCACCTTAAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAAGTCTCTAAGACATTAACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANANGAAAAAATGTTGATGATACCT GTTTAATTGGGAAATATGTTTGCATAT
WI-3564b	177	C T ---	---	---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACCTAAATGTTTGGAGAAATAAAAGT GAAATCAATGTGTCTCCAGTGTATTCACATGGCAGAGTGTACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCAGTGTGACTAACGTTAACATGCATGCTGTCTGTTCTTACAAAGTGTTTGTGGTGTCTATC AGTGTACACATGCTACCTTCCTTCACAAAAACAAA
WI-3564	177	C T ---	---	---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACCTAAATGTTTGGAGAAATAAAAGT GAAATCAATGTGTCTCCAGTGTATTCACATGGCAGAGTGTACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCAGTGTGACTAACGTTAACATGCATGCTGTCTGTTCTTACAAAGTGTTTGTGGTGTCTATC AGTGTACACATGCTACCTTCCTTCACAAAAACAAA

WI-3649	64 A ---	---	AATGTCCATGCTGTGACTGACCTGTCTAACACCTTTCCTAGTATTCCTTTAGTGGAAGATTCCACAG[G] AGACCAGTTTGCCTTCACTTAGTAGGGCCAAATAGACTTTTAGGTGCTACCAACAGGGTACCTGC ACAGCCACATCATATGTCACAGTATGGTTGCAAGGACCTGTCTAGACTCTTCTGCGCTTGGTC TTCTGTTTTACCATAATATGATGACATGCAACCTCAGAGCCTTTTA
WI-3674b	133 GC ---	---	ACAGTACACATGCCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCTCTCTAA ATTTAACTACCAGGCGGAGTGCTTTTATAGTAATTAATAATATGTTATTTAGAAAAATAACAAAATIG /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATGTAACCTGGTCAAAATGATTGTT AATCTTAATTAATTGTTTATGTTTNNATTACTGCCAATCACAGCCAAG
WI-3674	133 GC ---	---	ACAGTACACATGCCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCTCTCTAA ATTTAACTACCAGGCGGAGTGCTTTTATAGTAATTAATAATATGTTATTTAGAAAAATAACAAAATIG /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATGTAACCTGGTCAAAATGATTGTT AATCTTAATTAATTGTTTATGTTTNNATTACTGCCAATCACAGCCAAG
WI-3682	137 GA ---	---	CAATATAGACCAAAATGACTGCCACAAGAGAAATTAGTGGATCTACATTTAGAACCCACATGTTTTT ATTGGCTCTCTCTTCTCTCTCTCTTTTAAATGCTCTCTCCACACCAATTCACTTTATCTTTTCAA TIG/AJAGCATTTGTCCAAATTTAAAGTCAATGAAAAATAATGTACATTTTTTCAACAAGTATACATTA GCCCTGCAAAAGTCTTATGCTAT
WI-3854b	194 GA ---	---	GGTATGTTGAGGTCAGCTAATGGTCAGTGGTTTGGAGTGAATCTAAATGGATTTTTTGGCCCTTGA CAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCCTCCTTAGGCTTCTTGATTAACTC TGGTTCAGGAAGGCAAGGCGAGTTATGACCACCTTACAACCTGAGGAAATCAAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGTTTATAACAGAGTCAGAGCCA
WI-3854	194 GA ---	---	GGTATGTTGAGGTCAGCTAATGGTCAGTGGTTTGGAGTGAATCTAAATGGATTTTTTGGCCCTTGA CAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCCTCCTTAGGCTTCTTGATTAACTC TGGTTCAGGAAGGCAAGGCGAGTTATGACCACCTTACAACCTGAGGAAATCAAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGTTTATAACAGAGTCAGAGCCA
WI-4039	210 GA ---	---	AGCCAGCCACATCATGTTGAGTCTGCTCATCTTCCATCTCTTATTTCTCTACTGCCCTTCACCTT CCATTAAACAAGAACTCTTGATTACATTGTATGTTTGGTTACACTACAGAATCCAAGATGACCTC CCCATCTCAAGGTCAACTAATTACACCTTAATCTATTGCAATCTTTGTCAATACCATAACATATT CATGG[G/A]TTCTGGGATAAGGGGTAGACATTTTATGGAGGCCATTA
WI-4110b	130 T C ---	---	GAAAAATGATGTTTTGATTTCCCTTCCCTATCTTCAGATTATTGGAGTGTCAATTAGAAAACTGATAGT AACCTTTTATTTGATGAAACTCTGTCTATAATTAAACCTTCTCTCTCTCTTTATTTTGGCTT/CJACA GTTTAGGTAATAAAAGATGCCCAAGAAATTCAGTATTCAAGTACAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGAGGAGGTGNGGGGTTTTCTGGGAAGA

WI-4230	93 T	---	---	AGAGACGTTGAATGGGACATCTTTCTATTTCGATTTTAGTTTAAACATTTTGATAAGAAATTGATGAAA GTTTGTACATTCAGATTATCTTTATAGCAGCAGAAGTCTGGCAATAATAACAGCACACTGACT TTCCATGGTAAAAAGAGTTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATTCTGAAT ACATTTAAATGGAGGAGAAATAGTAGACCTTTGAAATTTTGAATTTATGG
WI-4241	118 CT	---	---	GAAATTCATTTGAAGTTTGACCTTGAACCTGATCTCAATTAATACTTTTNCCTGTAGTGGTTGATTT CATTTTGACAACAGAACAGACGAAAAATTCACCTTAAATTAATTCCTC/TJAAGTATCTATGAT TAGCACTGTTAGCACCAGAACTGTGAAATATCTCTAGATATCTTCAGAACTCTAGGATGGAAG AA
WI-4271b	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGAGCCCCAACCCCTCCCTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGAGCCCCAACCCCTCCCTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 GA	---	---	AATCGAAACATTGATTTTGTAAAGGAACACATTATTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAGAGAGAGATAGAAAGGATATTATTCATACCTTTTGG AGGTAAGATGTGAACCTATACA/GA/JNCGAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156 GA	---	---	AATCGAAACATTGATTTTGTAAAGGAACACATTATTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAGAGAGAGATAGAAAGGATATTATTCATACCTTTTGG AGGTAAGATGTGAACCTATACA/GA/JNCGAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31 A G	---	---	GATGACAAATTATTGTGATTGGCATTTTAAAG/GGTACCATCCATTTTCTCTGGCTTTCTGGTGT TGTTGTTGAGAGTCAGGGTTAGTCGTATTGCTCTTTCTAGTCTTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAAATTG TATTATCTATGCTTAAATGCTCAG
WI-4491	145 G C	---	---	ACCATCAATGTATCACCTTCTAAAAATTTATAGATGATTAACTGGCTCTGTTAAAAATAAAAAACCT GTCTTGGACATTGAAAAATAAACATTACTATTGGTCAATTTTCTGCTACTTACAAAGGTACTGCACTA AACAAATTAAAG/GC/GTGTTTTGGAGGGGAAAAATCATAAAAATGCATAAAATTTCTACCAGTGTCA TTCTTGTCCCATAAATAAAATTTTACATGCCT

WI-4584	144	A G	---	---	TTGGTTGGCATTAGCCTCATAACAACATATTACAAATCAATATTGTTACTCTTATTTTACAAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTAGTCGAGAGCCAGATTGAACCCAGGAATCCATT CACCGGTAC/A/GTGTACCTACCTGGGTAAATAATGTTTAAATTAATCTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTGAATAAGGTGTGCTTTAATTGTTTATCAGTATGC
WI-4639	185	C T	---	---	TTCTGCATTGAATGTGTATGGTCAGACTTCAGAGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCATTATTCAGAGAGATCTCAGTTTAACTTCCAATCCACCAATTAC TGACCATATGACTTGGGGAACATATCTCACCTATCTGAGTCTGTATCCGCTCATCTTTAAATTTGTA AATTTTAAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
WI-5327	63	A	---	---	AAATGAATCCGCTTAGAGCAAATACCAGTAAGGGCTGGTGAGGATGGTGGCTGAGAGA/A/- JGATTACTCATAAAGCATATTATTTTATAAATATGGAATAATTAAGTAAATTAATTAATGTGAAT TGAGTTTGAAGTTGCATGAGAGTAGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTTCGGATGACATGATGAATGTTCTAAGCAGACAG
WI-5390	87	C T	---	---	GCTTTTGAGAAATGAAAAGGGGAGCCTGGACCATTCAGGGCTCTTCATCTCTGATTATTTTGTGTAT TTATTGTTCACTTATTTATCTGTGTCTCTCCCTCTGTTGTCATGTCATGAAACAATGAATTC CCAGTGCCTGGCCGATTGCTGGCTCCTAGAGGTGCCAGAAAAAGTTTCGGTGAATAGAATTG ACGAATGGTTGAGAAATGAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G A	---	---	CCTTGCCTGCTTATGCATAATGAGAAATAGAGTTGACTCTCTGTCAGAAATCAATATTAAAGCAGT GCAACATTATTTAATTTG/A/JAAGAAACTTGTCTGAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTTCCACAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTCATAACAA
WI-5404	87	G A	---	---	CCTTGCCTGCTTATGCATAATGAGAAATAGAGTTGACTCTCTGTCAGAAATCAATATTAAAGCAGT GCAACATTATTTAATTTG/A/JAAGAAACTTGTCTGAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTTCCACAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTCATAACAA
WI-5545b	77	A C	---	---	TAGGAAAGGGGATGGTGGCTCTGAGACATTTAAATCTATCTTTTCCACTCACACTGCCGCCA TATCTCTC/A/CJCCAACACCTCTGTTTCTGACAGCCAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTATTTTCATTCA
WI-5545	77	A C	---	---	TAGGAAAGGGGATGGTGGCTCTGAGACATTTAAATCTATCTTTTCCACTCACACTGCCGCCA TATCTCTC/A/CJCCAACACCTCTGTTTCTGACAGCCAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTATTTTCATTCA

WI-5860b	134 A G ---	---	ACTCAAGTTGGGGGATAAAATCAGAAGTTTCTATGTACAACCTTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATTATGGATTTGTTTCTACCTCCCTAACCAACCTTCTAAGGAACTACAT GTTTACTGGAATCATGTGAAGACATTTCTAAAGGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-5860	134 A G ---	---	ACTCAAGTTGGGGGATAAAATCAGAAGTTTCTATGTACAACCTTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATTATGGATTTGTTTCTACCTCCCTAACCAACCTTCTAAGGAACTACAT GTTTACTGGAATCATGTGAAGACATTTCTAAAGGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-6106	208 C G ---	---	GCAAACAACCTATTATACCTGATTCCAAACCCAGGTCTACTAACATTAATCAACCCCTAACCAATAC TATATATTGCTGTTCTGAATTTTTCATTTAGAACTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGGCTCCAGGAGTCTCAATGTGAAGTATAATCTTACAGAG TAATTGATAGTAGGTCAACCAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129 T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTTC AAACCTATATTNCTGCTTGTGCATACCTTAAATGTATAATGTGGGAGAGAGAAATTTTGATG GNAAATATTCCCTGAAATTTTATACCA
WI-6109c	147 T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTTAA ACCCTATATTNCTGTCCTGTCATACCTTAAATGTATAATGTGGGAGAGAGAAATTTTGATG TGNAATATTCCCTGAAATTTTATACCA
WI-6109b	147 T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTTAA ACCCTATATTNCTGTCCTGTCATACCTTAAATGTATAATGTGGGAGAGAGAAATTTTGATG TGNAATATTCCCTGAAATTTTATACCA
WI-6109a	129 T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTTC AAACCTATATTNCTGTCCTGTCATACCTTAAATGTATAATGTGGGAGAGAGAAATTTTGATG GNAAATATTCCCTGAAATTTTATACCA
WI-6112	96 T C ---	---	AATGCTATCACCTCCATCATGCTGCATACTGATGATTCATATGCTTATTGTTAGCACCTGTC TTCCAAACACATGCTGTTTGTTCATGATGTCATATCCCAAGTCCCTAGACAATGCCCTCCCATAG AGTGAACAGTATTGACTAAACATACCTTGTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC

WI-6244	103 T C	---	---	TAATTGCACAACCTTACATATCAGGGTTCTGATTGAAAGGAAGAAATATTCCTTTCTTTAGTGATT GCTTAATATTAAATTCATAAATAGTGCACCATCTCTTCGCTCCTTATAAATGTGTTTGAAGAAGG AAATTGAGTGTTGGGAATTAAGCAACAGAGACATTTTATATACTCTACAGTGGGGAAGACTT CCTATTCTTTCCCAAGGATGGATACATTCTAC
WI-6268	124 C T	---	---	CTGGCCTTATAATCCAAAGTTAGGATTAACTTACCCCACTTAATAGACTCCAGACAGTTGCAGTT GTCTACAAGATTTCCTCTAGTAGGGCTTTGGGTGTGGCACCCTTTGGCTCATTC/TACTCTCCCT GGGTCTATTGACTTTCAGGGAGCTAGAAAGAGCTGGACAAACCTGCTCTTTTGCAGAAAGAGTCG GGGTCCAAAGATTTCGTTACGATTTTTA
WI-6336b	234 C T	---	---	AGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTACAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCAGTGCAATTATGTCTTGGTAGAGCC/TJTGAGGACACTGACAGT
WI-6336	234 C T	---	---	AGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTACAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCAGTGCAATTATGTCTTGGTAGAGCC/TJTGAGGACACTGACAGT
WI-6381	92 C A	---	---	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAGTTCAAAATAGTTATGAGTATTTATACAATTA CAAAAAATGNNTTTCATGTTTAAACA/CAGTATTTAAAGCTCAACATTTTAAACAGGCACAAT ATTCTAANGGCATATGGATTCACCATGGGCTTTGAATGTCTCACTCCCACTTCACAATCAAAATC TACAGANGGGCAAAAGATCAGAGTTTCAAG
WI-6436	198 C G	---	---	GGTTGAGGCATTGGGAAGGCAGAAATTTGAGGCAGTAGAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAATACAAAGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGTCATAAAGAAGTTAGACTTTGGTGGTTGTAGTAGTTGTAGTAGTAGGTAGCGTTTC GJATTGGGTGATTCACAGACAAGTGATGTTCTAAGATTGATATTATTGT
WI-6449	186 C T	---	---	GAGGCCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTGCTCAGACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTCTATTCTCATCTGCATCTCTGATCTTATGTCTGGCTCTATTCTATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCCTCTAAATTTTCTGTGGGTGATTATA
WI-6449	186 C T	---	---	GAGGCCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTGCTCAGACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTCTATTCTCATCTGCATCTCTGATCTTATGTCTGGCTCTATTCTATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCCTCTAAATTTTCTGTGGGTGATTATA

WI-6463	72 T C ---			GCTGGAGAGAAAGACCTCCAAAGAGAAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACAATTC/JTGAAAAAATTAAGTAGAACTCAAGAGAGCCAAAAAGTCCCAATTTGTGTCCATTA TAAGAAATATTTGAATGGAAATCTTAAGAAATGATTTTATTGATCAGTTAAATGTTCTTCTCTCTCTC CAGTCCCAITTTATGACATTCGCGCATGCTG
WI-6474b	76 C T ---			AAGCAGTAAATCTTCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/C/JGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGTACTAGAGGAGAACTATGTAAAGCAG AGGTATAGAGGAACCTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---			AAGCAGTAAATCTTCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/C/JGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGTACTAGAGGAGAACTATGTAAAGCAG AGGTATAGAGGAACCTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---			GAACCTCAATTAACCTTGCAACACTGAGAAAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCCGTGCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGTAA/GCTCCTTGTCAAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---			GAACCTCAATTAACCTTGCAACACTGAGAAAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCCGTGCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGTAA/GCTCCTTGTCAAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---			CACATTTTGAATGCAACTGAGAAANTGGTTTNTAGGCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGNTCCCAAGCCCA TTAGCAATATCTTA/G/AJTCAAATTTTAAAAAGAGAACAGGAAATAAGGAAGGCCTAACAGAGGAG TTAAATAATTGTGCAAAACCTTATCAGTTCTTC
WI-6564b	54 G A ---			TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCTCTATGC/G/AJCACTGGCTTG TAGGCATTACATCATATGTCTGTGCTGAAATCTCAATTAATTTCTCTCNCCTATTCTCTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGGAAGGCATTTGATTATNATTTTTTTTGGGTCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAAAATAAGACCAACA
WI-6564	54 G A ---			TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCTCTATGC/G/AJCACTGGCTTG TAGGCATTACATCATATGTCTGTGCTGAAATCTCAATTAATTTCTCTCNCCTATTCTCTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGGAAGGCATTTGATTATNATTTTTTTTGGGTCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAAAATAAGACCAACA

WI-6608b	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGTTC/- JAGTTGAGGAGCTAAAGGAGGGGATTTCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAGAAAAACACCTGTGCCCCAGGCACTAGCTACAAGGCCACACCAGAAAAAGGAA AGC
WI-6608	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGTTC/- JAGTTGAGGAGCTAAAGGAGGGGATTTCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAGAAAAACACCTGTGCCCCAGGCACTAGCTACAAGGCCACACCAGAAAAAGGAA AGC
WI-6666	68 C	A	---	GTAGACAGTATCCAGCAAAAAAGGTTATTTATACCTCTACTTTTCCAAACGAGGAAACCTCCCC A/C/AJAATCCCATCAACACACAGTCATGCTGGAAGGCATTTCTGCTTACTCTGTTGGTTTCATGTAA ATGTTGGGGTGAATCATTCGCTCTCTTCTTCTCAAGTTCAGGCTCTTGGGTAGACCAAACTA ATACAAATGTTAGGACACACAAGAGA
WI-6670b	120 A	G	---	AGATTAAACATAATTACTGGGGCCATTGTAGGGTTNGGAGGAGTGTCTTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GTTGTTAGCCA GCATTGCCATTGAGGGCCGAGTCAGGGTTGTGGGCCAGAGTTAGACAATTTGGGGAATCTGA AAAAAAAGAAATACAGAATTGTAAACACAGACACAGAACTTTAGAAGGGAT
WI-6670	120 A	G	---	AGATTAAACATAATTACTGGGGCCATTGTAGGGTTNGGAGGAGTGTCTTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GTTGTTAGCCA GCATTGCCATTGAGGGCCGAGTCAGGGTTGTGGGCCAGAGTTAGACAATTTGGGGAATCTGA AAAAAAAGAAATACAGAATTGTAAACACAGACACAGAACTTTAGAAGGGAT
WI-6704c	33 T	C	---	TTTGAAAAATAATTATGCACCAATGTTTAACTTCACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTTACAAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T	C	---	TTTGAAAAATAATTATGCACCAATGTTTAACTTCACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTTACAAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T	C	---	TTTGAAAAATAATTATGCACCAATGTTTAACTTCACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTTACAAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 G A ---			CCATGGACAGTTTAAATTAGGAAGCTTCGACTTGTAGAAATAACAGAGGAAGTCCAGTTATCTACCT ATTCTTAAACACACATTTTGTGAGGCTGGAATGATTCCTGAGTAAAGTCAACATCCACACCT GGATAAACATCGCTCCCAAGTGACTATTTACTGAGTCGACACAGGATGTCACCAGTGAGCCTC ATCTCAGTCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148 G C ---			AAACAAATGGTGCAATGCATAATTTGTGGTCACAGTATAAACAAATACAATTAGTTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGAGGNGAACTTACCAATCCAGTTCCTCTTC
WI-6766	148 G C ---			AAACAAATGGTGCAATGCATAATTTGTGGTCACAGTATAAACAAATACAATTAGTTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGAGGNGAACTTACCAATCCAGTTCCTCTTC
WI-6787b	97 A G ---			ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACTTGTGCAGCAATGTTCAAAATTCAC[AG]TTTTTACTGCATAGATATCTTCATGTACAACCTGT ATGCTTTGTCTCTTGGGAAGGACGCGTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTGCATAGGGCAGAGTAGANTACTCACAGGAAAAGAGTAAATTCAGGT
WI-6793	105 C G ---			GAACCCACAGGTCCTGTTATTTTAAAGGACATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGCGGCTCTCAAAATCAATCAGTCAACCCCTGAGAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTGGCTGTAGGAAGTAGGTTAATGCGCTTAATCCCGGAAAGGGCAGAGCTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAAGTTTCTCATCACAGGTAAAAGGCAAC
WI-6810b	37 T C ---			CACAATAATAAAATCACTCCCTACCTTGAACCTTTAT/CJAGAAGCATTTTTTAAATTTACAACACA AAGCTCAACGNACTACAATAAGTCTAGTCTGTTTACGNGCCCAAGGATAAGGCTGAACAATA AATTAACCCCTTAAAAATGTCTATGNACAAGTACAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---			CACAATAATAAAATCACTCCCTACCTTGAACCTTTAT/CJAGAAGCATTTTTTAAATTTACAACACA AAGCTCAACGNACTACAATAAGTCTAGTCTGTTTACGNGCCCAAGGATAAGGCTGAACAATA AATTAACCCCTTAAAAATGTCTATGNACAAGTACAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ---			GCATGATTAAACCAAGTCAGAAAATACCAAGTACATTTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACACATCATCACTAACAATGTAGCT GCAGGGTAAC[C/A]TGTGGATACCCCTGTGTGCTCTAGTNGCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTTTCAAAATCTTGGTTTCAGGTGCGGCTGTGTCAG

WI-6817	145	C A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTCACTCAACATGTAGCT GCAGGGTAAAC[C/A]TGTGGATACCTGTGTGCTCTACTNGCCTCCAAAGGCATTCAGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAAATCTTGTTTCAGGTGCGGCTGTGCAG
WI-6819b	221	C ---	---	GATGGAAGCCATTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAACATTTAGTAC CATCATGTACCCCTGAATGCCAGCAATACCTGACTTTTACACACGCGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTGCATATACAAAATTTTCTGCTATTTTG CTTAGCAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCAG
WI-6819a	175	G T ---	---	GATGGAAGCCATTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAACATTTAGTAC CATCATGTACCCCTGAATGCCAGCAATACCTGACTTTTACACACGCGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATT TTGCTTTAGCAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATAT
WI-6826b	154	A G ---	---	GCAAAAGCTTTATTGGCTCCAAACAAATATCCCTTTTAAACCTCCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTTTCAGATTTTCAGTTTATAGCATTTTTTCCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[AG]GAGCTTAAATAATATCAAAATGCAAAATAGATTGGTGCACTGT TAAGCTGAATTGCAATTTATGGCAACACACACTGGACTGGGTATAAGTTG
WI-6826	154	A G ---	---	GCAAAAGCTTTATTGGCTCCAAACAAATATCCCTTTTAAACCTCCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTTTCAGATTTTCAGTTTATAGCATTTTTTCCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[AG]GAGCTTAAATAATATCAAAATGCAAAATAGATTGGTGCACTGT TAAGCTGAATTGCAATTTATGGCAACACACACTGGACTGGGTATAAGTTG
WI-6857a	122	T C ---	---	AGTGCAAACTATTTTGAACAAAAGTAAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATATTTCACTAAGTAAATACAGCAGATGAGATGTCTCTCACATGTA[T/C]ATTTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTCAGTGTAAATTCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAAGTTTGGCAACTGTTTGGGCTAATT
WI-6865	153	G A ---	---	TTATAGAATACTTATGGGGCATACGNGTAAATGAACCTGTCAACCTTAAATCTAAACAACAGCTTG TTTGTGTTGCTGCTGAAATCCTCCCTGCTCAACAAACAGCCAGCTACTNGGTTTTCTAAAGACGTA ATTTGTCAGGCAAACTTC[G/A]TAGAGCCATTCCTGTGCAGAAAGGGAAGGAGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGGGCTGTTAGAACTGAGCTCATTA
WI-6909	73	C T ---	---	ATTGAAAACCTGGTAGCAACAGATAAATTACAATAGAGCCTGGATATAAAAATGAGAGAAGAATGC AGACTT[C/T]AAGCTTATAGAGAAAGTCAAAAAGGAGCAAGTTTTTGAAATCAGATTTTATGATAC GGAAAAAAATTTCCCTTTTGGCAACAGGATTTTCGAATAATAAATCTGCCAGTGCCAAATCAG AAACACCATTTCCACAATATTTCATGCCCCCTAGTTGCCCTATTTTATACATAIC

WI-6910b	163	G T	---	---	CACTCAAAACCCCTTTATTCATTGATTTACAAACTGTACAATATTTACAAAGTTTAGGCATTATATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATAGTTGAGATGTAAATGGAGAAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCACTCCCGGACCTTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144	A	---	---	GCTTGTTTTTTTGTTTTTTTAAAGTGACACCTTGGCCTTGGGCAATTTCTTCACCTTATCTTACCC AAAGTGCTTTGGGCCAGCCACTGACTGATTTAAACCAGAAATGTGGTTTTAAACAATGTGGT CGTGGTAATTCAGGTGATTTTCTATTGGTAGTATTTTCAGATTTCCACAAAGAACATG TATTGCTTTGTAATTTGAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175	T C	---	---	CAATCAAAAGTTCCAAAGTTTCAAGCTGGGATGAAAGCCAGGTCTTCTGACTTGCACCTCTGTCCAC ACTGGATTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCCATG CTTGCTTGGTCCCTGTGAGGAAAGGGTCAAGCTAAAGGT/CJAAGTGTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175	T C	---	---	CAATCAAAAGTTCCAAAGTTTCAAGCTGGGATGAAAGCCAGGTCTTCTGACTTGCACCTCTGTCCAC ACTGGATTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCCATG CTTGCTTGGTCCCTGTGAGGAAAGGGTCAAGCTAAAGGT/CJAAGTGTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79	G A	---	---	TTTTATGAACATTTTCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATCCCAATCCTAGGTAAAGTATCAAGTTACAAANTAC AAGTGCCGNTAAATTAACCTATAGGTAGTATATTAAACAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955	79	G A	---	---	TTTTATGAACATTTTCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATCCCAATCCTAGGTAAAGTATCAAGTTACAAANTAC AAGTGCCGNTAAATTAACCTATAGGTAGTATATTAAACAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6957	47	C G	---	---	AAACTAAAACCCCTTATTGTCTCCAAAGTGTGGCAAAATAGAAAATC/GJTTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATTCCTTAAGAACCATCCAGTCAATAATACAAAA ACAAATTCAGATTGCTTGGATCTTGGTCATTTATGGCTTGAAGAACTGGATTGAAAAACCACTTTAGG CTAAAATAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAAATCATGC
WI-6996c	242	G T	---	---	ACTTCTAGTGCTCTGTTACCAACCTCTAATGCCTCTGGTCCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGGTCCCTCTGCTCTTTCAGCAACCCAGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGAGGGGCTGCTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGAACCCCTGCTGACT CTCTCTGATGGTGGCCCTCTGTGCTCTTCTTCTG/GTTCGGATC

[illegible]

WI-7136	58 T C ---			TGTGAAGCCACATTTTCCAACATGAGCCCTCATGAAGCCAACTAAGTGTTATTGAAGCTGT/CJAATTC TCTCAATAACTCAGTGTAGCACTTTAAAGTCTGAAGGACAGCAACATGAAAAGAGCATATCAATGTG GTGGAGAAAGGAAGGGTTGGCTTTTAAATTTATTTCTTCATCTTTTATAACAAAGAAAGNNNNIN NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTAGCTTCTATATATG
WI-7146c	210 A G ---			GGGACGCCCTGTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTTTGCCCCCAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGGTCCCAACATGATGTGTGGCCCTCTCTCCGCATGCC ACGC/G/GIGTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7146b	210 A G ---			GGGACGCCCTGTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTTTGCCCCCAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGGTCCCAACATGATGTGTGGCCCTCTCTCCGCATGCC ACGC/G/GIGTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7146	202 A ---			GGGACGCCCTGTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTTTGCCCCCAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGGTCCCAACATGATGTGTGGCCCTCTCTCCGCAT/GA JCCAACGCAGTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7153	161 A T ---			ATATTACAACCTGCTTTTAGCTGATCTCCATCTCCTCAATGACTCTTTTCTTTTATATGTTAAACATA TATAAATGGCAACTGATAGTCAATTTTGATTTTATTTCAGGAAGTCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAAACNNNNNNIN/ATJAAAAAAGTTATTTAACAGTAATCTATTTACTAATTAT AGTACCTATCTTTAAAGTATAGTACATTTACATATGTAATGGTATGTTT
WI-7155	156 T G ---			TAGAATAGATGCGGTCAATTTCTTTGGCTTCTGGTTCTCCAGCCCTCATGTTGGCATCACATAT GCCGTGCATGCCATTAAACACCAGCTGCCCTACCCCTATAATGATCCTGTGCTCTAAATTAATATACAC CAGTGGTTCTCCTCCCTGT/GJTAAAGACTAATGCTCAGATGCTGTTTACGGATAATTATATTTCTAG TCTCACTCTCTGTGCCACCCCTCTCTCTCTCCCATCCCACTCCAG
WI-7169b	161 A G ---			AGCTCCACCAGATGCAGATTTGTGTTTGTGTTTCTTGTATCTACTGTACACAGCTTATAACATGTAT GCTTTTCAGAAATACAGTTGTCTAGCCCAAGCCCATCAAGTGTCTGAAATCAATATGGTTTATGCAAT ACAGCAAACCTTTTATTAAGTAGAT/GJGGAGAAATATGTTTAAAAATATTAGGAATCCTAGACCATA TTTTCAAGTCATCTTAGCAGCTAGGATCTCAAAATGGAAAGTTTATATATA
WI-7175b	194 C T ---			CTCCTAGACTAGTCTTTACCTTTTATTAATGAAGTGTGACAGAGGCCAAGCGCAGTGTCTCCTCACCA ATAACTTCAGAGAAAGTCAGTTGGAGAAAAATGAAGAAAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAAATATATAATGGTTTACTGCTGTGATTTGTCATGCCTA/C/TJAGAT AATTTATTTGTATTTTGAATAAAAAACATTTGTACATTCCTGATACTGGG

WI-7175	194 C T ---	---	CTCCTAGACTAGTGTCTTTACCTTTATTAACTGTGACAGGAAGCCCAAGGCAGTGTCTCTCACCA ATAACTCAGAGAAGTCAGTTGGAGAAAATGAAGAAAGCGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGCTGTCTGTCATTTGCCATGCCTA(C/T)JAGAT AATTTATTTTGTATTTTGAATAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273 G A ---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTGCTAGGGGAACAGACAGTGCACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTGCTGCACTAAGAGAAAATTCACCTAAATGAATCTGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273 G A ---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTGCTAGGGGAACAGACAGTGCACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTGCTGCACTAAGAGAAAATTCACCTAAATGAATCTGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116 A C ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGTGTACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACCAGTTCTCTGCAACCCACTCTGAGCCTT(A)CTCTCTCTCTCTATTT TACTTGAGGCTGCCAATACAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCTGAAGCCTAGTACCCCAATT
WI-7182	106 C A ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGTGTACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACCAGTTCTCTGCAACCCCA(C/A)CTCTGAGCCTATCTCTCTCTCTATTT TACTTGAGGCTGCCAATACAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCTGAAGCCTAGTACCCCAATT
WI-7191b	273 T A ---	---	ATAATTGCTTGTCTTAGCCTGGCAAGATATTTTCATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTAGATAAATGCACAGCACCACACCATCTAAGCATTAGTGATGGGTAGC TGATGTCAGCTTCATGTGGATTTAAGCACTCTAGAAACAATGAAGCTCTTGGCATAATTTAAGGAG CTCCCAAATGTGTACCTATTAAATTGTAACTCAGCAAGTAGAAGACCATTT
WI-7199c	112 T C ---	---	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTTGACCTATGAGCTCJGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTTGTTTTTGGTGCTCTGAAATTTCTCTTTATTAT AGTCTATAGTTTTACTCCTCAGTTCTCACCATCATCTTGCTCTAA
WI-7199b	112 T C ---	---	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTTGACCTATGAGCTCJGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTTGTTTTTGGTGCTCTGAAATTTCTCTTTATTAT AGTCTATAGTTTTACTCCTCAGTTCTCACCATCATCTTGCTCTAA

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WI-7233b	213	C T ---	---	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCGGGTCTGTTGTACATCCATTTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCACTAATATATTTAAATTTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTACTTCTTCTGCCACCTTTTGTGGCAATATTAAAGTGAAGTGTCTAATA GTGTAAGTAC/TGTGCACAAAACCACTGCCAGATAACCAGAGGGGCTG
WI-7233	211	T C ---	---	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCGGGTCTGTTGTACATCCATTTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCACTAATATATTTAAATTTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTACTTCTTCTGCCACCTTTTGTGGCAATATTAAAGTGAAGTGTCTAATA GTGTAAGTAC/TGTGCACAAAACCACTGCCAGATAACCAGAGGGGCTG
WI-7238	128	T C ---	---	GGTCTACAGACAGCTCAACATTTTGTCTGTATCTGTAAACACTTTTGTCTTAGTCTTTTCTTG TAAATTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGTTC/TCCGTT CTGTTTAAACAGAAATAAAGGAGTGAAGTCTCTTCTCATTTTCAAGTTGCTACCCAGTGAT GCAGTAATTAGAACAAAGAAACATTTCAGTAGAACATTTTATTTGCCTA
WI-7252f	520	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCTTCCACTGCGACGACGCCGGGACAGAG GCCTGCCCCGGGGCCAGCCCCGGGCTGGCTGGAGGCTGCCCCGGGCTGCTCTGCTGCTGCTG GACACTCTAGAGAACGACCCCTAGCCCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCACTAGACTCCTCTCTCCA
WI-7252e	552	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCTTCCACTGCGACGACGCCGGGACAGAG GCCTGCCCCGGGGCCAGCCCCGGGCTGGCTGGAGGCTGCCCCGGGCTGCTCTGCTGCTGCTG GACACTCTAGAGAACGACCCCTAGCCCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCACTAGACTCCTCTCTCCA
WI-7252d	540	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCTTCCACTGCGACGACGCCGGGACAGAG GCCTGCCCCGGGGCCAGCCCCGGGCTGGCTGGAGGCTGCCCCGGGCTGCTCTGCTGCTGCTG GACACTCTAGAGAACGACCCCTAGCCCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCACTAGACTCCTCTCTCCA
WI-7252c	552	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCTTCCACTGCGACGACGCCGGGACAGAG GCCTGCCCCGGGGCCAGCCCCGGGCTGGCTGGAGGCTGCCCCGGGCTGCTCTGCTGCTGCTG GACACTCTAGAGAACGACCCCTAGCCCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCACTAGACTCCTCTCTCCA
WI-7252b	540	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCTTCCACTGCGACGACGCCGGGACAGAG GCCTGCCCCGGGGCCAGCCCCGGGCTGGCTGGAGGCTGCCCCGGGCTGCTCTGCTGCTGCTG GACACTCTAGAGAACGACCCCTAGCCCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACCTCAGTCACTAGACTCCTCTCTCCA

WI-7252a	520 T C ---	---	---	CCACCAGGATCCAGCCCAAGGGGCCCTCCGGCCCTCCACACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGGCGGAGCCCGGCGCTGGCTCGAGGCTGCCCCGGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGAGCCCTAGAGCCTGCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACACTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252 T A ---	---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTGTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTTT/
WI-7265l	231 T A ---	---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTGTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265k	121 T G ---	---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTGTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265j	174 T A ---	---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTGTT/ATATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265i	227 T C ---	---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTGTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265h	80 T A ---	---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTT/ATATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTGTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265g	170 T G ---	---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTT/GTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT

WI-7265f	231	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTCAACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTT/AJAGGAGTAAAGATTGCGCT
WI-7265e	227	T C ---	---	AAC TTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTCAACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265d	174	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTCAACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265c	170	T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTCAACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265b	121	T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTCAACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265a	80	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTT/AJTATTTGCCACCAAAAGTAATGCATTTTCAACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATTATGTAAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7281b	183	C ---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCCAAGC ATCTTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCTGGCCCTGCCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGCATGAAGCATCTCAGACTCTTTCAGCAAAACGAGAGTCCGCGAGGCCGCGCAG GTGTGTGAAGACCACTCGTCTGTGTGGTGGGGTCTCTGCAAGAGGCCCTCCTC
WI-7281	171	C A ---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCCAAGC ATCTTCCCTGGGAAGTCTTCTGGCCAAAGTCTGGCCAGCTGGCCCTGCCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGCATGAAGCATCTCAGACTCTCAGACTCTCAGTGGCAAAACGAGAGTCCGCGAGGCCG CAGGTGTTGTGAAGACCACTCGTCTGTGTGGTGGGGTCTCTGCAAGAGGCCCT

WI-7282b	159	G C ---	---	TGTCACCTGGCACATTCTTCAGTTGAAGAAGAGAAAAATTTGAAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAGTGTTCACCTCAAAATATGTCAACTNNNNNNNT AGGCCCTTTCATAAAAACCAAACTG/CJT/AGCAAGATGCAATGCATGGCAAACTGTGCGGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACCAAGACAGTGTGAGATTGG
WI-7292	92	T C ---	---	CTTGATTACTCCACTGAGGTGGGAGCATCTCCAGTGTCCCAATTAATATCTCCCACTCCACTAC TCTCTCTCCACTTCATTTTCCJ/CJT/TTGTCCTTCTCTAATTCAGTGTTTGGAGGCCTGACTTG GGGACAACGTATTATTGATATTATGCTGTTTCTCTTCCCAATAGAAGAAATAGTCATGGAGCC TGAAGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A G ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGCGGTATGTTGTTGGTGGACAGGATATGGAA ACCAAGGTGGTGATATGTTGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTGJ A/GJCGGTAGTAACATACTATGTTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCA ATCAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301e	94	T G ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGCGGTATGTTGTTGGTGGACAGGATATGGAA ACCAAGGTGGTGATATGTTGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATACTATGTTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301d	138	A G ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGCGGTATGTTGTTGGTGGACAGGATATGGAA ACCAAGGTGGTGATATGTTGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGT/AGJTAACATACTATGTTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301c	211	A C ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGCGGTATGTTGTTGGTGGACAGGATATGGAA ACCAAGGTGGTGATATGTTGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATACTATGTTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAATCA AATTATGGAC/CJ/CATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301b	182	C T ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGCGGTATGTTGTTGGTGGACAGGATATGGAA ACCAAGGTGGTGATATGTTGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATACTATGTTGGTGGGAACATAATGATTTTGGAAAT/CJT/AGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301	88	G T ---	---	AACATATGGCAGTGGTCTGTTATAGTAGTAGAGCGCGGTATGTTGTTGGTGGACAGGATATGGAA ACCAAGGTGGTGATATGTTGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATACTATGTTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG

WI-7301	205 A C ---		AACTATGGCAGTGGTCTGGTTATAGTAGAGGGGGTATGGTGGTGGACCGAGGATATGGAA ACCAAGTGGTGGATATGGTGGCGGTGGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAATATGGTGGTGGGAACTATAATGATTTTGGAAATACAGTGGACAACAGCAATCA AATT/CTGGACACATGAAGGGGCGAGTTTGGTGAAGAAGCTCGGGCAG
WI-7314c	49 G A ---		CTCTCTTTTTTCTCAGATCTGCTCTCTGGGTTTAAATTTGGGAGGTCA/GJTTGTTCTACCTCACTG AGAGGAAACAGAGGATATTGCTTCTTTTGACAGAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTGGACCCAGGAAACAGCCATGTGGGTCCTTCTGTGCACATGAACGCTTCTTCCCGAGGA CAGAAATGTGTAGTCTACCTTTATTTTTTATTACAAAACTTGTTTTT
WI-7314b	49 G A ---		CTCTCTTTTTTCTCAGATCTGCTCTCTGGGTTTAAATTTGGGAGGTCA/GJTTGTTCTACCTCACTG AGAGGAAACAGAGGATATTGCTTCTTTTGACAGAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTGGACCCAGGAAACAGCCATGTGGGTCCTTCTGTGCACATGAACGCTTCTTCCCGAGGA CAGAAATGTGTAGTCTACCTTTATTTTTTATTACAAAACTTGTTTTT
WI-7314	36 A G ---		CTCTCTTTTTTCTCAGATCTGCTCTCTGGGTTTAA/GJTTTGGGAGGTCA/GJTTGTTCTACCTCACTG AGAGGAAACAGAGGATATTGCTTCTTTTGACAGAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTGGACCCAGGAAACAGCCATGTGGGTCCTTCTGTGCACATGAACGCTTCTTCCCGAGGA CAGAAATGTGTAGTCTACCTTTATTTTTTATTACAAAACTTGTTTTT
WI-7321b	199 C T ---		ACTCAGGGAAGGGATGCCCATTAAGTGACAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGCGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGTGGCACACCCATC[C /TGTTGCTGGGGTGTGGCAGCCACATCCAAAGTGGAGCAGCGCTGGCCA
WI-7321	199 C T ---		ACTCAGGGAAGGGATGCCCATTAAGTGACAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGCGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGTGGCACACCCATC[C /TGTTGCTGGGGTGTGGCAGCCACATCCAAAGTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C ---		AGACATTCTCGTTCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAGTGGCCTGGC TCCAGTGAAGTGGGCACATGCTCAGGCTACTATAGGTCCAGAAGTCTTATGTAAAGCCTGGCAG GCAGGTGTTTATTAATAATCTGAATTTTGGGGATTTTCAAAAGATAATATTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGCGAGCAACCTATAAATCA/CA/CJA
WI-7336c	221 A G ---		CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTGCTTACCTTGAGC CATTAATTTGTGCAGAGAAACAAAGAAACAGAAATCAATATAAATCAAGACTATCTGCAGCTA GTGTGTTCTCTTTACACAC/AGTATACACACAGACATCAGAAAAATCTGTT

WI-7338b	125 A C ---	---	CTGTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTGCTTTTAC/CCTTG AGCCATTATTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAAATTCGT
WI-7338	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTGCTTTTAC/CCTTG AGCCATTATTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAAATTCGT
WI-7338	221 A G ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTGCTTTTAC/CCTTG AGCCATTATTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAAATTCGT
WI-7384c	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGTATTTCATTGTGAACAGGATTTCTTCA CAGATCTCATTTT/AJAAAATTCCTAATGATTATTTTATTACTACTGTTGTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384b	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGTATTTCATTGTGAACAGGATTTCTTCA CAGATCTCATTTT/AJAAAATTCCTAATGATTATTTTATTACTACTGTTGTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384	145 T A ---	---	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGTATTTCATTGTGAACAGGATTTCTTCA CAGATCTCATTTT/AJAAAATTCCTAATGATTATTTTATTACTACTGTTGTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7388c	106 A T ---	---	TGAAATCCTGGGTCTCTGGCCCTGCTGTAGCTGTTTATTTTACTTGGCCCTCCCACTTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGGACTA/TJAAAGGTTTTGAATTCAGATTTAAAA ACCAACTATAAGCATTGCAACAAGGTTACCTCTATTTCGCACAGCGTCTCGGGATTGTGTTGA CTTGTGCTGTCCAAGAACTTTTCCCAAGATGTGTATAGTTATGG
WI-7388b	106 A T ---	---	TGAAATCCTGGGTCTCTGGCCCTGCTGTAGCTGTTTATTTTACTTGGCCCTCCCACTTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGGACTA/TJAAAGGTTTTGAATTCAGATTTAAAA ACCAACTATAAGCATTGCAACAAGGTTACCTCTATTTCGCACAGCGTCTCGGGATTGTGTTGA CTTGTGCTGTCCAAGAACTTTTCCCAAGATGTGTATAGTTATGG

WI-7388	94 T A ---	---	TGAAATCCTGGGTCTCTGGCCTGTCTAGCTGGTTATTTTACTTTGCCCCCTCCACATTTTTT TGAGATCCATCCTTTTATCAAGAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAA ACCAACTTATAAGCATTGCAACAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGCTGTCTGTCGAAGAACTTTTCCCCCAAAGATGTGTATAGTTATGG
WI-7438	64 A G ---	---	TTAGATTTTAAATTGGCAACCAGCAACTCACTGCCACCATTCACATGCAGATCTNCTATTCTCTGG[A/G] GTTGATATGACAAGGAACCTATTGGAACCAAGTCTTCAGATTGTCAGATGTCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTCTCACTGTAAACATAGTTTGTCGTTGTTGTTA TTGGAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152 T C ---	---	CCATGATCCCCCTCCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGCCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCAATTTGTCTACTTCTCAAAATGTTTTTGACA
WI-7454	152 T C ---	---	CCATGATCCCCCTCCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGCCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCAATTTGTCTACTTCTCAAAATGTTTTTGACA
WI-7464c	177 G C ---	---	AATTTGAAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAAATGCATAAATCTACTATTTATAATTTCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAAGCAGTTGCCA/GC/CAGAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAAAGCAACGTTCCACCAACAATTAT
WI-7464b	168 C A ---	---	AATTTGAAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAAATGCATAAATCTACTATTTATAATTTCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAAGC/AJAGTTGCCAGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAAAGCAACGTTCCACCAACAATTAT
WI-7464a	103 C A ---	---	AATTTGAAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAAATGC/AJACTAAATCTACTATTTATAATTTCTAT GTACAACAGAGCCACAGCACAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAAAGCAACGTTCCACCAACAATTAT
WI-7499b	134 T G ---	---	CAATTCCTCAATCCAACTAGTCTGTNTGCCCTAAACCATTCAGAGACAACTCCACTTCGAAGGTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGTCTCTTTGAATGCTTCAJT /GJTATAGTCTCTTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGA ACTCTGTACAAAAATCCCTTTTGAAAAATATAAATTTTGAAATGAGTGATGA

WI-7499a	33 A G ---	---	CAATTCTCAATCCAACCTAGTCTGTTGCTTAAGTCCATTCAGACAACTCCCACTTCGAAGGTT TAAATGCATAAGTCAGATAGCAATCTTCAGTTGCCAGAGGCACATCAGTTCTTTGAATGCTTC ATTATAGTCTCTTCAATTTAGCAATCAGTGAGGCAATACACTGGCATCATGCCCTTTTATAGGAA CTCTGTACAAAATCCCTTTGAAAATATAAAATTTTGGAAATGAGTGATGA
WI-7506b	118 A C ---	---	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAGTGAAAT GCATCCAGCAGCAGACCACTTNAAGTAGTCTGGTGGTGCCTAGC/CAGGAGAGTTGAG TGCCACAGGTAAGAATGAGTGAAGAGGAAATAATCATGATGTCATGATGCAGTAATTACTATGTCA GAAGAAAATATTTAAATAATTGGACCACCTCTTGTCTACCATCCCTACCCACT
WI-7506	118 A C ---	---	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAGTGAAAT GCATCCAGCAGCAGACCACTTNAAGTAGTCTGGTGGTGCCTAGC/CAGGAGAGTTGAG TGCCACAGGTAAGAATGAGTGAAGAGGAAATAATCATGATGTCATGATGCAGTAATTACTATGTCA GAAGAAAATATTTAAATAATTGGACCACCTCTTGTCTACCATCCCTACCCACT
WI-7534b	143 C T ---	---	TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTCTTGATGTTCCGAGTGTCACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAACACATCCCGGTGATAGAAATGCT AAATTGTCTGTGAATAGGTTAGAAATTTTCTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---	---	TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTCTTGATGTTCCGAGTGTCACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAACACATCCCGGTGATAGAAATGCT /CJAAATTGTCGTGAATAGGTTAGAAATTTTCTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---	---	GGGAAAGAAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCACTTGAAGGAAGAGTCTAAGAGTGAAGTAGGTTGACTTGAAC TAGATTGCATGCTTCCCTCTTGTCTTGG/AGGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCTCTCTGGCTCTTGGATGATGTCAGTTA
WI-7543	162 G A ---	---	GGGAAAGAAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCACTTGAAGGAAGAGTCTAAGAGTGAAGTAGGTTGACTTGAAC TAGATTGCATGCTTCCCTCTTGTCTTGG/AGGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCTCTCTGGCTCTTGGATGATGTCAGTTA
WI-7555c	60 T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAAATTTGTAGAGGTTCTCTA AAAAAGAGTGGTATGTTGTGATGATCAGCACTAAGTCTCGATTCCTGTAAAGCCACTTGGGTC ATAAGAAGGGAAGTAAATAAGAGTGTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCAATTTGAATTTTCAG

WI-7576b	168 A T ---	---	---	AATGATGATGATAATGATGATGACGACGACAAACGATGATGCTGTGTAACAAGAAAAACATAAGAGAGCCTTGTTGTTACAGTGTAAAAATTTTGAAGGCGGTACTAGTTCAGACACTTTGGAAAGTTTGTTCTGTTTAAACCTGGCATCTGACACAAAAAATGTTGAAGGCTTATCTACATTTCACTTACCTTTTGTAAAGTGAGAGAGACAAGCAAGCAANNNNNNINNAAGAAAAATAAAC
WI-7577g	77 T C ---	---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTGTTGCTTTCTTTAAATAATGCAATCJCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 G C ---	---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTGTTGCTTTCTTTAAATAATGCAATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---	---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTGTTGCTTTCTTTAAATAATGCAATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---	---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTGTTGCTTTCTTTAAATAATGCAATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---	---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTGTTGCTTTCTTTAAATAATGCAATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---	---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTGTTGCTTTCTTTAAATAATGCAATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---	---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTGTTGCTTTCTTTAAATAATGCAATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---			<p>AACATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTACTTTCTCTGAGGGTTTGTAGTA/GIACAGTAGGAGTTAAT AAAGAAGTTCAITTTGGTTACACGTAGGAAGAAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC</p>
WI-7577i	77 T C ---			<p>AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAITTTGGTTACACGTAGGAAGAAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC</p>
WI-7577h	50 G C ---			<p>AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA TAAATATGCATCAAAATCGTCTCTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAITTTGGTTACACGTAGGAAGAAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC</p>
WI-7577g	157 G A ---			<p>AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AGAAAGTTCAITTTGGTTACACGTAGGAAGAAGAGCATCAAAAGTGGAGATATGTTAACTAT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC</p>
WI-7577f	48 A G ---			<p>AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA TAAATATGCATCAAAATCGTCTCTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAITTTGGTTACACGTAGGAAGAAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC</p>
WI-7577e	84 G A ---			<p>AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAITTTGGTTACACGTAGGAAGAAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC</p>
WI-7577d	93 T C ---			<p>AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAITTTGGTTACACGTAGGAAGAAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC</p>
WI-7577c	154 C A ---			<p>AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AGAAAGTTCAITTTGGTTACACGTAGGAAGAAGAGCATCAAAAGTGGAGATATGTTAACTAT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC</p>

WI-7577b	117 A G ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTCATTTCTCTGAGGGTTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCTGTTATACATGACACTCTTCTGAATTGACTGTATTTTC
WI-7577	107 G A ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTCATTTCTCTGAG/GJAGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCTGTTATACATGACACTCTTCTGAATTGACTGTATTTTC
WI-7619q	106 C G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTC/GJCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTTCCATCTTTTCCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTTCCATCTTTTCCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTTCCATCTTTTCCCTC CGCTTTCTTTCTTACACAGAAACATTA/GJACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTTCCATCTTTTCCCTC CGCTTTCTTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619m	99 C T ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG TGCCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTTCCATCTTTTCCCTC TCTCGCTTTCTTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTTCCATTA/JCTTTTCCCTC TCTCGCTTTCTTTCTTACACAGAAACATACATACCGAGAAACCTATTTC

WI-7619k	90	C G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCG[C/G]CTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206	T G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCT[G/T]TCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106	C G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150	T C ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228	A G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTCTTCTTACACAGAAACAT[A/G]CACATACCGAGAAACCTATTTC
WI-7619f	237	G C ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99	C T ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG TGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189	T A ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---	---	---	ACAAGCGGACTTGAAGAGGACGCGAGCTTCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCC/C/GCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAATGGGGCCTCTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTCTACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	---	ACAAGCGGACTTGAAGAGGACGCGAGCTTCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT CGCT/GTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	---	ACAAGCGGACTTGAAGAGGACGCGAGCTTCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGC/GJTTAAACCATCATCTGGACCAAAATGTG CCATACTAATGATGAGCATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCTGCTGTATTTATAGTAACCATTTTCTTTGGAGCTGTTCA
WI-7626c	155 C T ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATCTGGACCAAAATGTGCCA TACTAATGATGAGCATTTAG/C/TJACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCTGCTGTATTTATAGTAACCATTTTCTTTGGAGCTGTTCA
WI-7626b	28 T A ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATCTGGACCAAAATGTGCCA CCATACTAATGATGAGCATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCTGCTGTATTTATAGTAACCATTTTCTTTGGAGCTGTTCA
WI-7626	144 T C ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATCTGGACCAAAATGTGCCA TACTAATGAT/C/GAGCATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCTGCTGTATTTATAGTAACCATTTTCTTTGGAGCTGTTCA
WI-7689c	134 A G ---	---	---	TCCATAACCGCTGATTCTCAGGCTCTGTCTGCTGCCGCCCAACCCAGATGGGGAAAGCAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTTAGAGCCACCCAGCAAAAGGTTGTCTCTAAAJA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAAGAGAGCTTAAT GATAATATTGTGGTGGCCACAAATAAAATGGATTATTAGAAATTCATATGAC

WI-7689b	134	A G ---	---	TCCATAACCGGTGATCTCAGGGTCTCTGCTGCGGCCCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGTCTGCTGCCAGGCCAGACCTCTAGGACGCCACCCAGCAAAGGTTGTTCTCTAAVA /GTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGGTGGCCACAAATAAATGGATTTATTAGAATTTTCATATGAC
WI-7689	121	G A ---	---	TCCATAACCGGTGATCTCAGGGTCTCTGCTGCGGCCCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGTCTGCTGCCAGGCCAGACCTCTAGGACGCCACCCAGCAAAGGTTGTTCTCTAA AATAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGGTGGCCACAAATAAATGGATTTATTAGAATTTTCATATGAC
WI-7690	45	G A ---	---	TGGAGAACATTCAATCTTCCGTCACATAATCAATGAAGATTAG/ACACTGAGATCCAGAGAGG CTGGATGACTTCTCAAGTTCCAGCATGTGTAGTGCAAGAGAGGTCCAGAGTCTGGCCCTTGAT GCCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGATGTTCCAGTGATGAGGCCACCCAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACCTGTCAGTTTCATCC
WI-7703b	164	T C ---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTTCACATTGGAACAAGTCAGTCATTGATATGATTCAAA TGCTATAACCAAACTGATGTAAAGTAAAT/CJGGTCTCTCAGTTGTTTATTAACTCTAAATTCT TTCATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7703	156	T C ---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTTCACATTGGAACAAGTCAGTCATTGATATGATTCAAA TGCTATAACCAAACTGATGTAAAGTAAAT/CJAAAGTAAATGTTCTCTCAGTTGTTTATTAACTCTAAATTCT TTCATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---	---	TAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGTTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/CJCCAGGAGTCCCTGGTAAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAAGGA GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCCAGCAGCTCTCAGCC
WI-7743d	275	C T ---	---	TAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGTTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/CJCCAGGAGTCCCTGGTAAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAAGGA GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCCAGCAGCTCTCAGCC
WI-7743e	106	C A ---	---	TAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGTTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/CJCCAGGAGTCCCTGGTAAATAAGTACT GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAAGGA GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCCAGCAGCTCTCAGCC

WI-7743d	275 C T	---	---	TTAAATGAGTGTGTTGTCAOOGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAITCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTATCCGAGGCAGGGTTCAGGAGAG GGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106 C A	---	---	TTAAATGAGTGTGTTGTCAOOGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAITCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTATCCGAGGCAGGGTTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCCAAG
WI-7743d	275 C T	---	---	TTAAATGAGTGTGTTGTCAOOGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAITCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTATCCGAGGCAGGGTTCAGGAGAG GGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743c	106 C A	---	---	TTAAATGAGTGTGTTGTCAOOGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAITCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTATCCGAGGCAGGGTTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743b	275 C T	---	---	TTAAATGAGTGTGTTGTCAOOGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAITCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTATCCGAGGCAGGGTTCAGGAGAG GGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	106 C A	---	---	TTAAATGAGTGTGTTGTCAOOGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAITCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTATCCGAGGCAGGGTTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743	275 C T	---	---	TTAAATGAGTGTGTTGTCAOOGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAITCTGCTACCTCACTGGGTCTGGGCTCGGAGCCTATCCGAGGCAGGGTTCAGGAGAG GGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7758	144 A G	---	---	TGACATTTATTCAAAGTTAAAGCAACACTTACAGAAITATGAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTTCAGAGTCTTCAGAGACTTCGTAATTAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC[AG]TAGTTTAAACATGCAATTATAAATTTTATAACAGAAATTAAGTAGATTTTAAAA GATAAATGTGAATTTTGTATATTTTCCATTTGGACTGTAACGACTGCC

WI-7765b	126	G C ---	---	---	ACAGGGCCTTTGGCAGGTGCAGCCGCCACTGCGCTTTGAACCTGCCTCCCTCATGCATGGAATTCCTCTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAGGGTCAGTATGG(GC)TTAGGGAAACATTCCTCCTTGAGTCAAAAAATCTCAATCTTCCCTATCTTTGCCACCTCATGCTGTGTGACTCAAACCAAATCACTGAACCTTTGCTGAGCCTGTAAATAAAAGGTCGGGA
WI-7773b	237	C G ---	---	---	TTAATTACTGATTCCAGCAAGACCAAATCATTTGTATCAGATTATTTTAAAGTTTATCCGTAGTTTTGATAAAAGATTTTCTCTATCTGTTCTGTGTCAGAGAACCTAAATAGTCTACTTTTGCCATTAAAGGCACTAGAGGTTTCATGTCTTTTACCCCTTNNNNNNNNNTTGTAAAGTCTAGTTACCTACTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAA(C/G)TTTCGACGTTTGA
WI-7774b	170	T C ---	---	---	TGCAACCTCTTTTGTGATGGCAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGACGGCACCCAGAATCAGATCCAGCTTCGGCATTTGATCAGACCAACAGTGCTGTTTCCGGGGAGGAAACACTTTTTTAAATACCCCTTTTGCGAGGCACCACTTTAATCTGTTT(C)ATACCTTGCTTATTAAATGAGCGACTTAAATGATTGAAAATAATGCTGCTCTTAGTAGCAAGTAAATGTGCTTGCT
WI-7785c	165	G ---	---	---	GCAGAGACCTTCCAAAGGACATATTGCAGGATTCTGTAAATAGTGAACATATGGAAGTATTAGAAATAATTTATGCTGTAAATCTGTAATGCATTGGAATAAACTGCTCCCCCATGCTCTATGAAACTGCAACATTGGTCAATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATCACATTTACCAATAATTTATTTGTCCATTGATGATTTATTTTGTAAATGTATCTTGGTGCTGC
WI-7785b	165	G ---	---	---	GCAGAGACCTTCCAAAGGACATATTGCAGGATTCTGTAAATAGTGAACATATGGAAGTATTAGAAATAATTTATGCTGTAAATCTGTAATGCATTGGAATAAACTGCTCCCCCATGCTCTATGAAACTGCAACATTGGTCAATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATCACATTTACCAATAATTTATTTGTCCATTGATGATTTATTTTGTAAATGTATCTTGGTGCTGC
WI-7785	156	T ---	---	---	GCAGAGACCTTCCAAAGGACATATTGCAGGATTCTGTAAATAGTGAACATATGGAAGTATTAGAAATAATTTATGCTGTAAATCTGTAATGCATTGGAATAAACTGCTCCCCCATGCTCTATGAAACTGCAACATTGGTCAATTGTGAATANNI- /JNNNNNNNGCCAAAGGCTAATCCAATTATTATTATCACATTTACCATAATTTATTTGTCCATTGATTTATTTTGTAAATGTATCTTGGTG
WI-7789c	84	G A ---	---	---	TCCTCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCCACCATCTTACAGAGACTCTCCCTGACCGGTGGAAATTTAA(G/A)TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGACCCAAAATGTGAATGAAGCTAATGTGAATGTGAATGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATATGCCCTCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7789b	84	G A ---	---	---	TCCTCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCCACCATCTTACAGAGACTCTCCCTGACCGGTGGAAATTTAA(G/A)TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGACCCAAAATGTGAATGAAGCTAATGTGAATGTGAATGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATATGCCCTCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT

WI-7789	73 GA ---	---	TCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGCGCACCATCTTACAGAGAGTCTCCG TGACG[G]ATGGAATTTAAGTTTAGGGTCCCTAAAGCAATTTGACACACAGTTGTTGATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTACGGCCGCTGCCCTAGGATAT GCOCTCCTGGTACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7790b	190 CT ---	---	AATTGTCAGTCACCTCTTCAAAACCTTACAGTCTTCTAAGGTACTCTTCATGAGATTCATCCATT TACTAATCTGTATTTTGGTGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G]TTTCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190 CT ---	---	AATTGTCAGTCACCTCTTCAAAACCTTACAGTCTTCTAAGGTACTCTTCATGAGATTCATCCATT TACTAATCTGTATTTTGGTGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G]TTTCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81 CA ---	---	CAGATGTTCTGGTAAAGTGATTGCTGGCAACACAGATTCCTTGGCTCATATTTCTTTCTCAT CTTGATGATGAT[C]A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCOCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTCCAGAAAAATCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7795	81 CA ---	---	CAGATGTTCTGGTAAAGTGATTGCTGGCAACACAGATTCCTTGGCTCATATTTCTTTCTCAT CTTGATGATGAT[C]A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCOCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTCCAGAAAAATCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7814c	41 GA ---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCC[G]ATTTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTTGTATATTTAAGAAATAACAGAA
WI-7814b	41 GA ---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCC[G]ATTTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTTGTATATTTAAGAAATAACAGAA
WI-7814	28 GA ---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCCGTTTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTTGTATATTTAAGAAATAACAGAA

WI-7830d	150 C T ---	---	---	GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTATGTC/TTAAATGTACACATTGCAATTTGATAAAATTAATTTGTTGTTTCCCTTG AGGTTGATCGTTGTTGTTGCTGCACTTTTACTTTTTGCGTGTTGGA
WI-7830c	54 G A ---	---	---	GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTATGCTTAATGTACACATTGCAATTTGATAAAATTAATTTGTTGTTTCCCTTG AGGTTGATCGTTGTTGTTGCTGCACTTTTACTTTTTGCGTGTTGGA
WI-7830b	134 G A ---	---	---	GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGAAC G/AJATCCATAACTTATGCTTAATGTACACATTGCAATTTGATAAAATTAATTTGTTGTTTCCCTTG AGGTTGATCGTTGTTGTTGCTGCACTTTTACTTTTTGCGTGTTGGA
WI-7830	44 A G ---	---	---	GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTATGCTTAATGTACACATTGCAATTTGATAAAATTAATTTGTTGTTTCCCTTG AGGTTGATCGTTGTTGTTGCTGCACTTTTACTTTTTGCGTGTTGGA
WI-7865e	25 C T ---	---	---	CCACTTCCTATCTGATTTTCCAG/C/TAATGAGGCGAGGCAATTCCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCTACCTATACAACAAGCTAGCTATTAGAGGGTGGTTGGG GGTATGCTACTCATAAGATTCAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCCACCCAGTAAACCCAAA
WI-7865d	191 C T ---	---	---	CCACTTCCTATCTGATTTTCCAG/C/TAATGAGGCGAGGCAATTCCTAGTCTTCCACAAAACATCTA ATCTAAATGGAGAGATGAATCTACCTATACAACAAGCTAGCTATTAGAGGGTGGTTGGG ATGCTACTCATAAGATTCAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCCACCCAGTAAACCCAAA
WI-7865c	25 C T ---	---	---	CCACTTCCTATCTGATTTTCCAG/C/TAATGAGGCGAGGCAATTCCTAGTCTTCCACAAAACATCTA ATCTAAATGGAGAGATGAATCTACCTATACAACAAGCTAGCTATTAGAGGGTGGTTGGG ATGCTACTCATAAGATTCAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCCACCCAGTAAACCCAAA
WI-7865b	191 C T ---	---	---	CCACTTCCTATCTGATTTTCCAG/C/TAATGAGGCGAGGCAATTCCTAGTCTTCCACAAAACATCTA ATCTAAATGGAGAGATGAATCTACCTATACAACAAGCTAGCTATTAGAGGGTGGTTGGG ATGCTACTCATAAGATTCAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTCCACCCAGTAAACCCAAA

WI-7865	25	CT	---	---	CCACTTCCTATCTGATTTTCCAG(C/T)AAATGAGGCGAGGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAGATTTGAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAACCCCAA
WI-7865	191	CT	---	---	CCACTTCCTATCTGATTTTCCAGCAATGAGGCGAGGCAATCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTGAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTA(C/T)GAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAACCCCAA
WI-7867c	92	AC	---	---	TTCAACACCTGTCTCCACCTCCACCATCTGTGCAATCACTTCACTTCACTTCCAGCTCAGTCCCTC CTAACAAATACCTGTCAAGAGG(C/G)GAGTGAGCTCAGGTGATTTAATGTGGTTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92	AC	---	---	TTCAACACCTGTCTCCACCTCCACCATCTGTGCAATCACTTCACTTCACTTCCAGCTCAGTCCCTC CTAACAAATACCTGTCAAGAGG(C/G)GAGTGAGCTCAGGTGATTTAATGTGGTTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173	CT	---	---	TTGATCGATCTTTCCACCTGTGCTCACTCAACGTGTGCTCCTAGAACAGAGGCTTAAACCGGGCTTT CAOCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTTCCAGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGCTTACCCCTATTCAAGCA(C/T)TAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTTCATTCTAATGCCTAGAT
WI-7868b	173	CT	---	---	TTGATCGATCTTTCCACCTGTGCTCACTCAACGTGTGCTCCTAGAACAGAGGCTTAAACCGGGCTTT CAOCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTTCCAGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGCTTACCCCTATTCAAGCA(C/T)TAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTTCATTCTAATGCCTAGAT
WI-7868	66	TC	---	---	TTGATCGATCTTTCCACCTGTGCTCACTCAACGTGTGCTCCTAGAACAGAGGCTTAAACCGGGCTTT /C/T)CACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTTCCAGTCTCCATCTCAGTACAC AATCATTTAATATTTCCCTGCTTACCCCTATTCAAGCA(C/T)TAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTTCATTCTAATGCCTAGAT
WI-7870b	85	TC	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAGAAAGCACTATTAATACTCTGCAAGTATTAGAAGG GTGGGGTGGCGGAATCC(C/T)ATTATCAGACTCTGTAATGAATATAAATGTTTACTCAGAGGA GCTGCAAAATGCTGCAAAATGAAATCCCAATGAGCACTAGAAATTTTAAACATCATTAATGCTCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG

WI-7870	76 C T ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCAGCTATTAATACTCTGCAGTGATTAGAAGGG GTGGGGTG[C/T]GGGAATCCTATTATCAGACTCTGTAATTGAATATAAATGTTTTACTCAGAGGAG CTGCAAAATTCCTGCAAAATGAAATCCAATGAGCACTAGAATATTTAAACATCATTACTGCCATC TTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C ---	---	---	TTAGGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGGTGCAGGACTCTAGCTCATGAGTGGAAGTCACTACAGGACTGGCGGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAGGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGTCTCTCCAGAGCACAAGAAAG
WI-7889b	54 C ---	---	---	TTAGGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGGTGCAGGACTCTAGCTCATGAGTGGAAGTCACTACAGGACTGGCGGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAGGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGTCTCTCCAGAGCACAAGAAAG
WI-7894c	142 A G ---	---	---	AGCCACCCCAATATACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACTTATGTCCTATTGTTTGTGAATTTATATTGCGTATAC ATTATC[AG/T]ATGTAAAATTGCAATTTTTTATTGAAAATTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAAACCGCTATAGAGTATTCATA
WI-7894b	142 A G ---	---	---	AGCCACCCCAATATACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACTTATGTCCTATTGTTTGTGAATTTATATTGCGTATAC ATTATC[AG/T]ATGTAAAATTGCAATTTTTTATTGAAAATTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAAACCGCTATAGAGTATTCATA
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGAOCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC
WI-7900d	128 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGAOCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGAOCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC

WI-7900d	128 C T ---			---	GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAACAACAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGA AACACAGTGATTAAGTTTGATCAAGCCCATGGTGAIC/TJACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAAA TATGATGTATTTCTGAGCTAAAACCTCAA CTATAGAAGACATTAAAAGAAATC
WI-7900e	84 C T ---			---	GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAACAACAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/CJTCTGCCATTGA AACACAGTGATTAAGTTTGATCAAGCCCATGGTGAIC/A AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAAA TATGATGTATTTCTGAGCTAAAACCTCAA CTATAGAAGACATTAAAAGAAATC
WI-7900d	128 C T ---			---	GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAACAACAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/CJTCTGCCATTGA AACACAGTGATTAAGTTTGATCAAGCCCATGGTGAIC/A AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAAA TATGATGTATTTCTGAGCTAAAACCTCAA CTATAGAAGACATTAAAAGAAATC
WI-7900c	84 C T ---			---	GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAACAACAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/CJTCTGCCATTGA AACACAGTGATTAAGTTTGATCAAGCCCATGGTGAIC/A AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAAA TATGATGTATTTCTGAGCTAAAACCTCAA CTATAGAAGACATTAAAAGAAATC
WI-7900b	128 C T ---			---	GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAACAACAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGA AACACAGTGATTAAGTTTGATCAAGCCCATGGTGAIC/TJACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAAA TATGATGTATTTCTGAGCTAAAACCTCAA CTATAGAAGACATTAAAAGAAATC
WI-7900	84 C T ---			---	GCTCACTGTGACCCATCCTTACTCTACTTTGGCCAGGCCACAGTAACAACAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/CJTCTGCCATTGA AACACAGTGATTAAGTTTGATCAAGCCCATGGTGAIC/A AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAAA TATGATGTATTTCTGAGCTAAAACCTCAA CTATAGAAGACATTAAAAGAAATC
WI-7901c	33 C T ---			---	AGACTTAGGTACAATTGCTCCCCCTTTTATATA/CJTAGACACACACAGGACACATATATTA AACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACA AACTCCAGGCCCTTGGTTGGGGTGGCTGGGTTATTGGGGCAGCGCCGCTGGTGGT CACTCAGTCGCTCTGCATGCTCTCTGTGCATACAGACAGGTAACCTAGTTC
WI-7901b	33 C T ---			---	AGACTTAGGTACAATTGCTCCCCCTTTTATATA/CJTAGACACACACAGGACACATATATTA AACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACA AACTCCAGGCCCTTGGTTGGGGTGGCTGGGTTATTGGGGCAGCGCCGCTGGTGGT CACTCAGTCGCTCTGCATGCTCTCTGTGCATACAGACAGGTAACCTAGTTC

WI-7901	33 C T ---	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATA[C/T]AGACACACAGGACACATATATTAACACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACTCCAGGCCCTGGTTCGGGTGCTGGTTATTGGGCGAGCGCGGTGGTGGT CACTAGTCGCTGCTGCTCTCTGTCATACAGACAGGTAACTAGTTCT
WI-7901	271 T G ---	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAACAGATT GTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGACCCCT TTTTAAACAACTCCAGGCCCTGGTTCGGGTGCTGGTTATTGGGCGAGCGCGGTGGTGGTGCAC TCAGTCGCTGCTGCTCTCTGTCATACAGACAGGTAACTAGTTCTGTGT
WI-7926c	150 C A ---	---	---	CATTCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCAT TACAATGCAATACCTTA[C/A]ATTTTAACTCTGTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926b	28 A T ---	---	---	CATTCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCAC ACTTTGGAGATCAGAAAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCCTTC ATTTACAATGCAATACCTTA[C/A]ATTTTAACTCTGTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926	150 C A ---	---	---	CATTCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCAT TACAATGCAATACCTTA[C/A]ATTTTAACTCTGTAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7947b	203 G T ---	---	---	AAGGCCAGCAGGTCAAAGGCCAACACACCATAAGCAGCCAGCCACACAGGCCAGGTCTCTGT GCTATCAGAGGTCACTCTTTACAGTTAGAACACCCAGCCGAGGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAATAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTTCGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGGCGAGCCAGTGTGCCACCTG
WI-7947	203 G T ---	---	---	AAGGCCAGCAGGTCAAAGGCCAACACACCATAAGCAGCCAGCCACACAGGCCAGGTCTCTGT GCTATCAGAGGTCACTCTTTACAGTTAGAACACCCAGCCGAGGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAATAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTTCGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGGCGAGCCAGTGTGCCACCTG
WI-7963b	145 T C ---	---	---	CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAGTAAGACTAATTTTAAAAATAAAATGCC ACAAATTTCAATTTCTCTCTAAGTATTACAATGGAGTTATTCTGCGCTAAAAAGTGAAGAAAT TGAGTGAATGAT[C/A]ATTTTGTAATTTAGGATAAGATCCAAGTTATTTCCCAACTCTTTGTTTCC CCATAAAGTTAGGCATGAGGAGGAGCAGCTATTAAAGGCAGAGACGGGAAAA

[illegible]

WI-8021b	57 C T ---	---	ACAACTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATTCATCTGGAAC[C/T]GATCCC ACGCTTAGAACCTTACCACAAAGGAGTTTCTTGTAGTGATTCTCAAGTCTTGGTAGGCATTGGA ACTGGTCTTTACATTTGAGATTTCTTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTTAGGGGTGATTGCAATTCGGTGAATTGCCA
WI-8021	57 C T ---	---	ACAACTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATTCATCTGGAAC[C/T]GATCCC ACGCTTAGAACCTTACCACAAAGGAGTTTCTTGTAGTGATTCTCAAGTCTTGGTAGGCATTGGA ACTGGTCTTTACATTTGAGATTTCTTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTTAGGGGTGATTGCAATTCGGTGAATTGCCA
WI-8024c	206 A G ---	---	CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTACGAGGACAGGACAGGATCCAGTGGCCTTCCATGGGAAGACAGAGAGAGT GGGCCACAGAGATGGAAGACCCAGTGTCATCACCACAACCACTTCAGCCGCTCTAGCCTCTAA TTCCG[A/G]CTCTAGAACAGCTGGCCCTGGTGTGTCAGTACACAAGGAAGAGC
WI-8024b	206 A G ---	---	CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTACGAGGACAGGACAGGATCCAGTGGCCTTCCATGGGAAGACAGAGAGAGT GGGCCACAGAGATGGAAGACCCAGTGTCATCACCACAACCACTTCAGCCGCTCTAGCCTCTAA TTCCG[A/G]CTCTAGAACAGCTGGCCCTGGTGTGTCAGTACACAAGGAAGAGC
WI-8077	167 A G ---	---	GAATGAGCCTTCTAGCCGAGGAGCTGCTGCTGTTGTTGGCTGCACATGCATTCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCCAACTCCTTTCT AAGGAGCTGGGGTGTATGCCCTACAAACG[A/G]TAAATTTCTATCAGATGGATTATTTAATTAACGTT GTGATTGTGACTTACTTTCCAACTGACTCTGGCATAACAAGGGAAAAA
WI-8118f	114 G C ---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGATGAGCTTGT[G/C]TTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40 A G ---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGATGACCCTCCCTTGCTAAGGAAGC TATGTAATTCATGCTGTGGAACTGGCAATACAGATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118 T G ---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTGGATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---			TCTAGGTTTAAATCAAAAGCAATTGTCANTTTGGATTTTGGAAATGAIC/TJCACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAAACTGGCAATACAGAAATGTAGCTTGTTTGTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCTCTTCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTTAAATCAAAAGCAATTGTCANTTTGGATTTTGGAAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAAC/TJGGCAAAATACAGAAATGTAGCTTGTTTGTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCTCTTCTTCTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAATGCCAGCGGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGCAAGAGACACAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/TJGTGGCAGCGGCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAGAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGACACAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 A G ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/TJGTGGCAGCGGCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAGAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGACACAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 T C ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAATGCCAGCGGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGACACAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCATTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGGG/CJAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAATTC TGTGATGATGAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCCT
WI-8314	78 C/G ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCATTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAATTC TGTGATGATGAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCCT

WI-8321	178	G A	---	TTTAAATATGCCCGTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTATATACTGAGTCTCTGAGAAG TCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAJG/AJAGTATCTTAGTATCTTTCTA TTTGTCTATGGTCTAGTTATCAACCTACTTTTATTAGCTGAACGTGTGGC
WI-8321	178	G A	---	TTTAAATATGCCCGTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTATATACTGAGTCTCTGAGAAG TCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAJG/AJAGTATCTTAGTATCTTTCTA TTTGTCTATGGTCTAGTTATCAACCTACTTTTATTAGCTGAACGTGTGGC
WI-8332b	123	A C	---	TATGTACTCACTTCAGTTACCCCGTGCCTCCAGAATCGCATGTTCCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGAGCCTTAGAJC/JACTAAGTAG CAGTACTGTTTGGTGTGTGTTTCTTCCCGAGCAATGCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C	---	TATGTACTCACTTCAGTTACCCCGTGCCTCCAGAATCGCATGTTCCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGAGCCTTAGAJC/JACTAAGTAG CAGTACTGTTTGGTGTGTGTTTCTTCCCGAGCAATGCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGAGGAGAAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATTAGA AACTGCCCCATGATCCAATCACCTNTCACAGGCCCCCTCTCTCAACACAGTGGGG
WI-8378	308	T C	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGAGGAGAAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATTAGA AACTGCCCCATGATCCAATCACCTNTCACAGGCCCCCTCTCTCAACACAGTGGGG
WI-8426	184	T G	---	TTTAGCACATATTTAGCATTAAAGCTCAACGATACAGCAATATGTTACATTTCTTGTGAAAAACAG TTGTTGTAGACTGTTAANNNNNNNAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNNTAA GAGNNTCTTTTCTGTGGGAGGGTGGCTTGTCTGAACCTTCCATCTGTG/GJGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGNCCCGGGGCCCTTGGCNATNGNATTCAGTGAG
WI-8450h	61	C A	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTC/AJCA TCTTCTATCTTAGTCCAGTTTATGTTTCAATCCCAATATACCAATTCATGTTATTTTAAAGA AAAAACCTTCCAGTTTATGTCAGAACTATGTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATAGAGCAGTACAGAGTCTTAATGCAATTCTAT

WI-8450g	55 T C ---			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATATACCAATTCATTGTTATTCJTTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATATACCAATTCATTGTTATTCJTTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATATACCAATTCATTGTTATTCJTTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATATATACCAATTCATTGTTATTTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATATATACCAATTCATTGTTATTTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAG AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A G ---			CAAGGAAAGTGTCAGTCTTCATAAACTTTCAAGAGTTACAAAAATACGTTATTTTAAAGJCTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGATAGTATCGTCACAGACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATACCTTGTAAGAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTTATAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---			CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATATACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCAATTTTAA/NNNNNNNNNNCTTGCTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTAACACATTACAANTTTNTAGAAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---			CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAAT/CTATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAATCAATTTTNNNNNNNNNNCTTGCTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTAACACATTACAANTTTNTAGAAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---			CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAAT/CTATAACTACAACCTTACAAATGCCAATTA TTAGACAAAGAGANTAAATGATATAATATAATCAATTTTNNNNNNNNNNCTTGCTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTAACACATTACAANTTTNTAGAAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---			AATAACATGTTATGAACAAGCTGGTTACAAGTAGGTAGGTAGTAAATTTTGTATAAAAAAT TAAAAAGCAT/GJAAACATGCATATAAAAAATAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATAATCTCCCTTGTTTGTCTTTTAAAAAACATTATTTCTGAAAAA ATCAGAAAAACATGATCGTGGAGAGAAATTA
WI-9438	77 A G ---			ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTGATACAAAGTAACATTTTAGTA CAGAAAAATCCAGTCTGTGAGCTCAGTACCTGTCTGTGTGCACACTGTACCATCTCAGTCCACTCT GCCTGTAACCTAGAAAAACAGCCCTACCCCGAGAGGCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAAACAAAG
WI-9439b	101 C T ---			ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTGATACAAAGTAACATTTTAGTA CAGAAAAAT/CTCCAGTCTGTGAGCTCAGTACCTGTCTGTGTGCACACTGTACCATCTCAGTCCACTCT GCCTGTAACCTAGAAAAACAGCCCTACCCCGAGAGGCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAAACAAAG
WI-9439a	76 C T ---			GAAGGCTTGATTAAAGGGAGGNTTATTTGATGTNAACCTACCATCCATAGACTATAAAGANCATTA TAAAAAAAT/CTCCCTCTAAAGNGACACATGCCCAAATGACCANGNCATAAGCAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTGTGTCCTACTNTATCACTGTGCTCTGCTTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9446b	75 T C ---			

WI-9446	75 T C ---	---	GAAGGCTTGATTAAAGGGAGGNTTTATTTGATGTGNAACCTTACCATTCCATAGACTATAAGANCACTTA TAAAAAAATTCJCTCTAAAGNGACACATGCCCCAAATGACCCANGNCATAGCAAAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTTGNCCCTACTNTTATCACTGTGTCTCTGTCTTTTGTGTACCTTA TGNGAACTGCACACTATCTGTGGCAATATGT
WI-9497b	185 A ---	---	ATTAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATACATTTTTTT GAGATAATTTCTAGATTCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTAAATTAATCAAAAGTATGTTAATGTCACCT GGAATCTACATGGAAAAGCCAAACAAATAACTAAAACCTTGACTAAATGAAG
WI-9497	185 A ---	---	ATTAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATACATTTTTTT GAGATAATTTCTAGATTCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTAAATTAATCAAAAGTATGTTAATGTCACCT GGAATCTACATGGAAAAGCCAAACAAATAACTAAAACCTTGACTAAATGAAG
WI-9523b	193 C A ---	---	GTGAAAAAGTTTCTATTCTCATCATACAAATAGATTGTGCTAAGGATCATTTTGGAAAGATGTG CAGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGGTATTTTCCACACATTTGTAIC/AJAGTG AAAGCTCTTCAGCTTGGAAACAACCTTGTCAAGGCAGACTGCATGCACATATAT
WI-9523a	47 G A ---	---	GTGAAAAAGTTTCTATTCTCATCATACAAATAGATTGTGCTAAGGATCATTTTGGAAAGAT GTGCAGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTCAAGCCATGATCTATGGTATTTTCCACACATTTGTAIC/AJAGTG AAGCTCTTCAGCTTGGAAACAACCTTGTCAAGGCAGACTGCATGCACATATAT
WI-9554	202 T C ---	---	AAAAACAAAGTTTCATACATCACAAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGATACTGCCTTNTAGTTGTTATTGTACAAATGCTGTAGATAATGCAGGCCCATG CAATACCCCAAGAACACTAGAGTCCTACACCCCAAGTACATATGATAAAGCAGCCCTCTGCAAGTG GTTCJGCTGGATACCCTAAGAAAGTCTACTGCAGCCATGTTGTTAIGATTTT
WI-9555	97 G A ---	---	CCAAAAGCCAAACCATTCATATGATGGATTTTCATAAACATTTATTGATCCTTTTGTAGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC[G/A]CTTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCCAAATGATCATACTTCAGATTAAAAACAGGTAAGTATTCAG GGNTAAAATGGTACAAAAAGGCTGTAACCTTTTNTCTCAGATTGATCACA
WI-9625b	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCTGGGAAAAACCTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGTTGTGGACAAGTTACTTCTA/TGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172 A T ---			TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACATAGCTACCATAATTTGTATCTNCTCCTGGGAAAAAATCTTGGAAAAAATCAACACGACACA TAAGTATCATAAAGTGGTTGGGACAAAGTTACTTCTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTTCATTTAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---			TTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTATGCTACTATACCTTTTTTCATCCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTGTATGCTAGACCTAAAAATCCAAGCT TACAACTTC/TGTCTTTACCTGATACATTTATTCCATTTACTTTCATTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGCCCTGCTTTTGTAGTTAATTGTGTTT
WI-9676n	114 A G ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676m	184 G T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676l	84 A C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676k	202 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676j	92 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676i	173 T C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTGCCCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCAATGTTGTTT

WI-9676h	134	C A ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCC C/AJATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676g	202	C T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG C/TJGAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676f	184	G T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676e	173	T C ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676d	134	C A ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCC C/AJATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676c	114	A G ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676b	92	C T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676a	84	A C ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT

WI-9738b	40 C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA/C/AJTACAACTCATGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACAGATAAATGACTCCACATTTTCCCTTT GAGTCAACAAAGACTCTGCTTGTCACCTTGCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCTTATGTTGGTGGGCACATGCTGTATTGCTGTCC
WI-9738	40 C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA/C/AJTACAACTCATGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACAGATAAATGACTCCACATTTTCCCTTT GAGTCAACAAAGACTCTGCTTGTCACCTTGCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCTTATGTTGGTGGGCACATGCTGTATTGCTGTCC
WI-9756	47 A ---	---	ACTGAAATGTAAATGGCAAGGCCACCCAGGACCTTAAATCATAAGAAAGTTAATCTGTGGGAAAA GAGTAACCTACAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGTCCCTTATCACTTTAGTTC AGTAAGATAAGAAAGCCCTGGTGAGTATCCACTTCCACAAACACACAGAAATATACACTTTTGAAG ATTCCACTTAACCACTTGATTCTTCACTTTTTATGATTTAAAACTCTCCGTGG
WI-9758	135 A G ---	---	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAGAGGCTGAATGAATAAT TAGGAACTGGGAGAAATTCAAATTCAAAGAAAGAAATTTCTGTCGAAGTCAATTTTATACTATTTA A/GJTAAATAAATCTGCTGAGTTCTATAGCAAAATGCTAAGTAAAGTAAACCGCTGTTTCTAAAT ATTACG
WI-9778	127 G A ---	---	ATTTAAATCCAGGCAGCGGGGAAAAATGGATACTTTTCATATGCTCTGTACCCAACTATAAACTTTTG GTTCTCATGCACCATTTTCAATTTTGCTTCTCACTCCAGTACCAGTATTTACCAATTG/AJCTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTGAATTTGGAAATTTCTATACACACTTTGCCTCA AAGAAATGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A ---	---	TCTCCCTTTGCCTCTCATGCCCCTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGCTGACAATGCAGTTTTC/AJTGGATCCACCCAGGA CTCAAAAACCTAGGAATTGGGAGAGAGGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAGTGGACTAAAGTTTGAGGACACAGACATGGAAGGTGGCTTTGGC
WI-9841	101 A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCATTTTGAATGAATAAATATAC/AJGTGTGTATGATATATATATCTTATTAAACACTT AGGATTATATACACACAATAAACGCTGTGAAGATAAATAAGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTTGTTACTTGATATGCTGTG
WI-9880c	222 G A ---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTATTGGCAGTTAAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGGTGGTTTTTATGATATCTCCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATTTTATATAAGCACATGAA AATGGAATGAAATAATGA/GAJTTGACATAGGAATACCTACATATTTTG

WI-9880b	157	C A ---	---	---	GAACAAACACCTTTCTTGCATGGATTTTCTTGATTTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGA/C/ATATAAGATCCTCTTTTAAATATATATTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T ---	---	---	GAACTAACACCTTTCTTGCATGGATTTTCTTGATTTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATATTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T ---	---	---	ACACTGCAGGCACCTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTATTTTAAAAACAACGCCCCAGTTATCACAGTTCTNTTTTTGTC/TJ/CACC ATTTCCATAACAAAAGAAGCTACACAAAATTNGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCACAAA
FB25G10b	109	A G ---	---	---	TCCCTCAATGACAGATGAACATAATTTCTCTTGGGTGAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA/J/GTGATTTTAGATCCTCCCCCAG TGACAAGTAACTGAACTGACCATAATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
FB25G10	109	A G ---	---	---	TCCCTCAATGACAGATGAACATAATTTCTCTTGGGTGAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGA/J/GTGATTTTAGATCCTCCCCCAG TGACAAGTAACTGAACTGACCATAATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
IB3071	102	C A ---	---	---	ACAACGCTGAACCTTCCATAACAGTCAATGGTACAGTCAAAACATCACATGTACAGAACACACAATTTA GATGAACCTGAAATTAAGNTAAATAAAATAAAATJ/C/A/CAATTTTCAGNAACAAAAATCAAAAC ATTAAGNITCCCTGNINATATCTTAACCCCTAATGAGATTTCACTGNNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCTATTAAACCCAGTCTAGGGATTCTG
NIB551	161	C T ---	---	---	CGTCCTTTCTTTTGGATTTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATTTGGGTTGTCCO TACTGAGCTTGGGGCCAGGTGTACTTAGGAACCCCAATCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGTCTCTTGAACACATACATCGGCCCATTTGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAACCAAAAGCTTGTCC
S72904	51	G T ---	---	---	AGCATAGAAAGTGATTTATATTTTAAATGGTTTCAAGTGAAGTTCCCTTTG/JAATTTGTGAGTTC ATTCCTGGAAAATCTTTTGAGTTAAATAAGGATCCTAGGACAGCACCTCGAACCTACAGGCCCTAAA GAGAAATTGCCTCAACCAAGTGTGTAACCTCTCCCTCTTCTGTCAATGGTTGCTCTTAAATA TTGCAAAAGTCTGTGCTAAACAGTATTTGGAGTGTTTTCAGTGTCTGTGA

UTR-00481	115	CT	---	---	TATCTTTTATCTGGGGCCACAGTTCTTGATTATTCCTCTGTGGTTAAAGACTGAATTTGTAAACC CATTGAGATAAATGGCAGTACTTTAGGACACACACAACACACAGA[CT]ACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTCGTTTGGACAAAAATAACNAGAGGCATCCACGGGATTAGTTA GCCATCAAAATTTCCCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC103	21	---	---	---	
ESTC107	20	---	---	---	TGCTGGCTCACTTCCTCACANGCTGTATTACCTTTACAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTTCCTTTAATTGTAAGCGGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCATATCACAAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAAATAACACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAGCCAGGCCCATCATNTCCATGGGACCCAGGCTGGCTCAA TGTGGAACCTGG
ESTC129	20	---	---	---	AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAAACNCATGTTGTCAGGTTTCTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTTGGCTTCTGTCTCCTCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	---	---	---	AGGACACAGCCTAAGGACATGAAGTCAGAGTTTCTCAGAGAGNGGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCATTGTGTGCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGAGGTAATAATCTATTTTATTCATTTTAAATC AAGANACCATTCCTTCTTCAACAACA
ESTC143	29	---	---	---	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTCCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTCTTGACATGAGGNGCTTTTAGCAGCATTTTCGG
ESTC146	20	---	---	---	CATGTCCAGGATAAGGAGCANACACCAGGATTTATACAGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTTGTCTACACAGACACTTAAGTACTGTATGCTGTNATCGAGGGCCTGTGGAGGCCCTG GGGGTGGCTGGGCCCTGTGTCTGAG
ESTC149	28	---	---	---	TCAGTTCAATTTATTTGCTTTAAGAGTTANATACCATGAGACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAAAACAAAGCACACANACTTATAGAATCTTTGGTTTAAAAATTTATCATAATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCATTTTCTTTTAAATACAAATCTACTGGTGTCTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAACTCATGAGCATTTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGAGCGCAAAACAANCTGGCTGCTCGGGATGGAGCGGGGGCGCCTCA CCACCACTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTCTGAGGCACATCAGNTACGTTGTGTCATTTAGGGCACGGTCTGGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCAGTGATCATACCCACAAGGACAGGTT
ESTC160	38	---	---	---	---	TTCTAGCATTGCTGGTGCACTGGGGGCTGAGCTGGGNGCAGTGGCAGTGTCACCTGGGCCGTTTG GGACTGGGTTGA
ESTC162	36	---	---	---	---	CTCTCGTCGGTTTGCAAGTTGCTGTTGTTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATTCTCCATAGAATAATTGGTTTTGTAAACANGAATACAATCCAATATATAACATTAAACAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCTCTGGTGTGCAGGGAATCANITTTGCTGGATTAGAGGAAAGGTCCGGCTCTGTTTCCATGACTT
ESTC176	23	---	---	---	---	CACTCTCCCTGAGCTACCCANGTAGTGTCTGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAAATTTTNGCTTATTCTATTAAATACCTTTTAT TCTCTTTATTTCCCATAAAAAGGCAACCAA
ESTC18	29	---	---	---	---	TCAGACACTGGGACATCAGCATTGTCTCTONTGTACAGCTCCCTTCCCTGCAGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTAAATAATAATACATATTCACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCTTGACTAGCGAGGCTACATCAACAATTTATAAAGTGCCAGATNAGTGCTAATTTGTCATTGAGCTTG ATTTTTCACCTCA
ESTC187	24	---	---	---	---	ACCATGATTGCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG TCTATTAAACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATCACTCATCACTTGTCTTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	---	TCCTCAATACCACITTTCCCTTAACATTATCAGTCTAGTAGCNTTTCAAAGGAGGAAAAATGGGTAC CTTTCAGGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGCTGCTCTCCCTCCNGCAAAGTCTCCCAAGCACA
ESTC20	33	---	---	---	---	AAGATTAGGACAGACCGCGTATAGTAAGCTCTGNGGAACCTCCAAGAATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAATCCCAATATATGAGTTTAAAAAAAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG

ESTC201	35	---	---	---	---	TCTTACTTGGGTAGTTAGCAAAACATTTTAAANCCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	---	CTGCTGGAGGAGGACAGACGNCAGCGGCTGGTGGCCGCCAGAAAAGCTGGCGTGATGTT
ESTC203	27	---	---	---	---	CGAGATGAGCC
ESTC208	43	---	---	---	---	ACACTTAACAGGTTAAATAATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTATTGTGCTAC
ESTC210	29	---	---	---	---	AAGACACGTTGCA
ESTC212	27	---	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATACTATTGTTAAAGC
ESTC214	21	---	---	---	---	CTAAGAGTGAAAA
ESTC216	49	---	---	---	---	GATGAAGTGGCTTCTTTGGCGAAAGGATNAGAAGTGAGTGACGGTGACCTGTG
ESTC217	28	---	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGT
ESTC219	32	---	---	---	---	TCAAAGTC
ESTC22	41	---	---	---	---	CTCCAGAGTCCCTCTCTCANACCAGGGGCAGGAGGAGTAGGGAAT
ESTC223	27	---	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTAATTAATCAGAGGTATNTTAGATTGGTCAGAAAA
ESTC224	37	---	---	---	---	CAAAAGACCA
ESTC225	20	---	---	---	---	TTTTGTGAGTAAATGAGCAATACACTGANTGGAATCTGCATGATTAATAACATTAACAAGTTTCAT
ESTC23	27	---	---	---	---	AAACACACCCCA
ESTC230	43	---	---	---	---	GTACACATCTGGGGTGAGCACACAGCAAANGGGTGGACGTGCAGAGAGGTATAGGGTAAAG
ESTC231	24	---	---	---	---	GCAAAGGAAGC
						TCATTGAAGAAAAATTATGGGTTTATTCTTATTCTAATTGNGAGAATGCTTAATGTCACAGGCTACA
						TAAGGGCC
						CTTCTGAAGCCCAAGAGAGGGGCAGANGTAGTCTTGATTTAAAAAACAGAAAGGGGAGGAGGA
						CGAAGGTAGATTCCCTCACATATTACAAAATACACANAACACACACACACACACACACA
						TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAGGA
						ATGTGTAGGATCG
						TTCTACTTTATTTCATATTTCCACCACNATAACGACTCTTTAAATTTAACTAAAAACCATACAGGGT
						TCCTGAAAGGG
						GCTTCTCCACGAATTTGAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
						CAAAAGGGTAGTCATATTCCCCCANCAACAGCATGATAAAATAATCAAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTTGTTCTCTATTCTCTATAAAATAAAGGAAGCAGAAATCT GC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCNGGCCCTCAATTCATATTTATTCTTGAGCCGCTTGGTCAGGTTTGAT TCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATAATTNTCAGTCGGTGATCATTTGTAATATACAATACAAAG CAATTTCTCTCAGA
ESTC33	25	---	---	---	AGCACTTCCAGCTCCTTGACGTTGNGGACCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAAGGGAACCCACCTGGGCTTTNGGTCACAGAACTCAGAGCCTGGGCATTAA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAATCATATTATGCTGATGGAAAGAAACCATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAATAATTTTGACTTTTCCCTCCAC
ESTC45	37	---	---	---	TTTGAGGTTTGTGCTGGAGTTTGTCTTTGTAACNCTCTCATCATCGAGGCTATATATAA
ESTC50	56	---	---	---	CTGTCCGTGTGAGCOCTGCGCTGTCCCTGAGGCCCCAGGAGCCACTGGTGGGANNCCGGGCAGATG TTTACCCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGCGTGGCAGGAAGNAGTGGAGGGAAGGACACCA AGT
ESTC57	20	---	---	---	AAGTGGGCCCTCCAGTCCCTCTCTGGGCACAGATCCCACAGTCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTGTTCCAGACTTCAGGAAAATGATTTCC ACATGTTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNITAGCTACTTTTCAAGATTGAAGGAGAAAAATGCATTATG TGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTTGGTAGCGGTGTTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACCCANAGGGCCCCACGGGAGGTGCGGGAGACGACACTTTTTCCTCGGAAA GGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGT CACTTTCGCTAA
ESTC7	45	---	---	---	AGTTTCCCTAGAGCTGTGCGGCCAGATAGCTGTTCTGAGTTGCANGCACCGATGGAGATTGGACACT G

ESTC72	37	---	---	---	GGGCTTCCAAATGGGTATTGGGGCCAGGAGGCTGGCNTTTGGCGTGACGCCTAAAAAGTGTGACC AACAAATTCACAGCTACAGGAAATCTAGAACAAAATCAAATATTCATCACNTTGGTTGAAAGTTG GAAGA
ESTC74	49	---	---	---	ATGACTTTCTGTCCTCCATCGGAACACAGAGTTTCCCCAGGNGAGCCCTTCTTAICTGGGGTTA
ESTC77	40	---	---	---	GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCTCCAGAGGGCAGCACTCCAG TTTCAGATGATGGGCTGAGATGTTCTCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC81	20	---	---	---	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC82	25	---	---	---	TTTAGCTGTATACCAAGTTTCCATAAANCTGTCTGTCTGGTGGGAGGCTACAGCCTGACCACATTCT TTTGC
ESTC83	53	---	---	---	ATTGCAAGGAAGTGGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC85	28	---	---	---	CTGGTTCTCTCGTCTGGCATTCCTCTCCTCNGGCCAGTCTCCACCCAAAGTGTCTTCCCGATGAT
ESTC89	22	---	---	---	CTCCCTCTCAGTTACAGTGGAGACTANGGAGATTACAGGCGAGGATCC
ESTC90	33	---	---	---	GCACGTTCTTTGTTCTCTCTCCAGAAGTTGNAGACGCTATTAGTTTGAATATCTGTCTG
ESTC93	29	---	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTCA GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTGACTGTTCTCCACCTGCCAG ATTCTTCAATGATCTTTCACCTAAGAAACAGCAAGATTCTGGCAAGCACAGGATCTAGAGATAC ATCTTATTGGGATTTTTCACAAAATCAAAAGAGAAAGGCTTAGCTG
DWU-100	127	CT	---	---	TTCCATCTAGATATCTACTCAAATAATTGAGACAAGTGTCAAACAGAAAGACGCTTGTGCTGAA TGTTTCATGGC[A/G]GCCCTATTACAGTAGCCAAAGCATGAAACAAACCCCAAGCTATATATACCA GATGAAAGGATAAACAAAATGTGGTCCATCCATCAATGGAGTATTACACAGCCATAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-177	77	A	G	---	CAAAATACCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATTCAAGGTTAATCCATCTAAGTGAC ATTTTGAATTCAGCGGTGCCACCAATCATGCCAGCTTCTGTCTATGAATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGGTCTGGAAACCCAGCCCTATCTGAGTCTTCGGTCCCTCC
DWU-286	213	A	C	---	

DWU-252	94 A G ---	---	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGCTGACAAGGCACCTTCATGTAAGTGT CAGAAAGGAGCTACAAAACCTACCCCTCA/GJTGAGCATGTAATCTGGCCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTTCTGTTGAATGACAAAGTATGTGGTTTTGTA AT
DWU-330	85 C T ---	---	---	GAACATTCCTCTGCAGCACTTCACTACCAATGAGCATTAGCTACTTTTCAGAAATTAAGGAGAAAA TGCATTATGTGACTGA/CJTCGACITTTCTAAAGCTCTGAACAAAAGCTTTTCTTCTTTTGCAA CAAGACAAAGCAAAGCCACATTTTGCAATTAGACAGATGACGGCTGCTCGAAGAACAATGTCAGAAA CTCGATGAATGTGTGATTTGAGAAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231 A G ---	---	---	GAAATGTTAATTGGGCAGGTGAAAGGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAGAG AAGCATCATTTCCCAACAGGCAACTGTAGAGGCCAGCTGAAGAGTAAGGAAAAGGCTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAGGTAATGTTGAGGGCCCTTCACTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCACTGTCTGTTCTT/GJGCACTATTTCCCTCTGTGC
DWU-1537b	89 A G ---	---	---	CTCTTAACCTCAGTTCCTCATCTATAAGAAATAGGGATTCAAGTTGTGATCACAATAGCTCAGGTAATC CAGGACCAGAAACCCAGGAGC/GJTGAGCCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52 C T ---	---	---	CTCTTAACCTCAGTTCCTCATCTATAAGAAATAGGGATTCAAGTTGTGATCACAATAGCTCAGGTA ATCCAGGACCAAGAAACCCAGGAGCATGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196 C G ---	---	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCAGCCAGAGGCCCTGGGGAATCCAGGGTCACTGTTCCCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTG/CJGAGA CCCGCAGACCAACTCTGAGCTTTCTGGGCCCTCTGAGTCTTGTCTC
ESTD-ADAA	184 G A ---	---	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCAGCCAGAGGCCCTGGGGAATCCAGGGTCACTGTTCCCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTG/GJGCACTGAGCTGCAGA CCCGCAGACCAACTCTGAGCTTTCTGGGCCCTCTGAGTCTTGTCTC
ESTD-ANT1	160 T C ---	---	---	TCCTCTGTCACTTCTACTCTCATTAGTTCAAGGTCAGTGAAGAACTGGGGCAATTAACCAAGTAATTCA TGGACTGCCCAACTGCGAAACAAGAGGCCGACGTGGAGCAGGAGTATTATGCTACGCGGTACCTT TTTTTATGGAGGACCGAACTGAGGCT/CJGAGCTCAGATGATCTCTGT
EST10398 2b	168 A G ---	---	---	TGCCTGGGTGGCAAGGCTGCAACAAGAGGCAACCCAGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTTACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTGTTTTCTCGGGCCAAAGAGGTATCTACCA/GJATAGTGTCTATTAGGCAATTG

EST10398 2a	147 C T	TGCCTGGGTGGCAAGGCTGCAACAAGAGGAGCAACCCAGGAGGCTTTTATGAAGGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTGGGGCTTGACCTTTCCACACGAGAGAAG CATTTGTTTCTTTC/TJGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
ESTD-C7	14 G C	ATATCGTGGCCTTA/GC/TACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C	CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACTTTCAAGG ATAATGGGGCAATCACTTCTTTT/CCTTCCTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A	AGTCTTCATCTGCGGTGTCAGGTAGATCCCTTTTCAACG/AJCCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G	CTGGGCTGCCCCGACGAGCTGCTGGCACTGGACGGCGCGCCAGGCTCACTCTATAGTGGGGTCG TATTCGTCCACAAAT/GTTCATCTGGATCAGCT
ESTD- HRASa	37 C T	CTGGGCTGCCCCGACGAGCTGCTGGCACTGGACGGC/TJGGCGCCAGGCTCACCTCTATAGTGGGG TCGTATTCGTCCACAAATGCAATCTGGATCAGCT
ESTD- NRAMP	81 A G	GGAGGAGGAGGTGGGAGGGGCTGCTGCTCCAGGTCACAGACCAGAGAGAGCGGCTCAGTG TATCCCAACCCCA/GJTGTTGGCGCTGGAGATGAAGAGGATGATGCAGGT
ESTD-OTC	18 A G	GTGACCTTCTCAGCTTAA/GJAAACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAAATTTAGGATAAAACAGAAAGGAGGATGTATAACA
EST36751 7	36 C T	CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACT/CJTGATTACTTTTCTATTCAAATCTCTGTA AAATTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	109 A G	CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTGCCCAACTGTGGCTGAC TTTATGGCTAAGAAAGTTTCTACCTGGATGCATTAATAACAATTA/GJTTTTACCTTTGAAAAATAA ATGAAGGATTTGACCTGCTTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTTGAAACAATACA GATGCTTCCCTTGTAGCAGTTTTCAGCCTCTCTACCCCTA
EST18288 3	121 C T	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGACGCTGTGACAGGATGGAAGACTGGCTGCCCTGA/CJTTGGAGCCAGT GTGGACAGCACCCCTGGCTTTCAACACCTAOGTCCACTTCCAAGGTAAGGCAACCTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATOC
ESTD-AK- 168	31 C T	GGGAGTGACAGCTAGACCAACCAAGGGGGGCT/CJTACAGCTGTGTCTCATGGAGGACAGGCTTCT GCTCATTTCTGG
ESTD-ALB	180 A G	AATCCCAGCACCTTTAGGAGGCTGAGGCGAGGCATATCACAGAGGTGAGGAGTTTGAGACCAGTCTGA CCAACATGGTGAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGTGCATGCCCTGT AATCCCAGGAGGCTGAGGAGGAGAAATCGCTTGAACCTGGGAGGCGIAGIAGGTTGTGGTGAGCCGA GATGGCAACATTGCACCTCCAGCCTGGGCAACAAGAGTAAACTCTGTCTTC

EST70523 3	182 G T ---	---	TTCCGCCAGCCCCCATCTTGCCACCCCTGGTCCCTCAGGGGCCACCCCGGGGCACTCACCGCTCT CGCTCTCGGTAAACATCCGGCGGGCGCGCTCTTGAGCACATAGCCTGGACCGTTTCGTATAGGAGG ACCGTGTAGGCCCTTCCTGTCCCGGGCCTTGCCAGGGGCCAGCCCTGTTGACAGAGAGGGGTCCCTGT GGTTGAGCTGAACACACAGCTGTGGAGTGTCTCCACGCTG
ESTD- APOA2	101 C T ---	---	CCAGGTGTTGTGGCACGTGCTGTATCCACAGCTACTCGGGAGAGCTGAGGCATGAGATCTTTTGAAC CGGGAGGCGGAGGTTGCAGTGAGCTGACATCGTC/TGCCACTGCACCTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---	---	CAGTGTATCTGAAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTACGATCTTTGGCTCACATGAAGGCCAAATCCGAGAGAC/C/TCTAGAAGATACACGAGAC CGAATGTATCAAATGGACATTACAGCAGGAACCTTCAACGATACCTGTCTGTAGGCCAGGTTTATA GCACACTTGTACCTACATTTCTGATTGGTGGACTCTTGCTAAGAACCTT
EST74167 6	137 C ---	---	AGACCATGAAGGAGTTGAAGGCCCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGCGGGCACGGCTGTCCAAGAGCTGCAGCGCGCCAGCGCCGCTGGCGCGGACATGGAGGA CGTCGCGCGCGCCCTGGTGCAGTACCGCGCGGAGGTGCAGGCCATGCTCGCCAGAGCACCCGAGGAGC TGCGGGTGCCTCGCTCCACTCGCAAGCTGCGTAAGCGGCTCCTC
EST43211 8	132 C ---	---	CGCTGTGTGAGTACCGCGGAGGTGCAGGCCATGCTCGCCAGAGCACCCGAGGAGCTGGGGTGGCG CCTCGCTCCCACTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAACGCGCC TGGCAGTGTACAGGCGCGGGCGCGGAGGGCGCGAGCGGCTCAGCGCCATCCCGGAGCGCGCTG GGGCGCTGTGTGAACAGGGCGCGTGGCGCGCGCGCGCTGTTGGGCTC
ESTD- AFSB	126 A ---	---	GGAAGAAATGGAGCCTGTGGGAAGAGGCGTCCGAGGGTGGGCTTTGTGGCAAGCCCTTGTCTGA AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGTGCCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCAATCAGTGAA GGAAGCCCATCCCCAGAAATTGAGCTGCTGCATAATATTGAOCCAAAC
EST36770 4	144 C ---	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTCCAGCTATAATCC ATCGAAATGTATTTTCAATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACGAAATAATATACTGGGTTTCTGTTTCTTCTGATCAT TCTTACAAGTTATCTTATTGGAAGGCCCTTAAAGAGGCTTATG
EST26021 1	137 A ---	---	TAATGTAAAGCTCATCCACCAAGAAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTCCGAAACCTGT CCATAAAGTAATTTTGTGAAGAAGGAGCAAGAGAACATTCCTCTGCGACACTTCACTACCAAAATGA GCATTAGCTACTTTTCAAGATTGAAGGAGAAATGGATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTCTTTTGCACAAAGACAAAGCAAGGCC
ESTD- BA511	29 A/G ---	---	GGGCAACATAGTGAAACCCCATCTCTACA/G/JAAATACAAAAATAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCAAGATGGTCCACTGCA

ESTD- CB22	119 C T ---	---	---	GGCAAGTTTTATTGATAGAGAGGAAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCACCCATAGGCTGAGGATACAAAAG ACAGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCT AGTAACATAATTGCTTCATTATGGTCCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C ---	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTTCCCGGCTTCTCTCAGACATACAGAGGCCCTACAGGACAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAAAAACGTGTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAAA
ESTD- CB24	145 A ---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGTCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAG GCCACACTGGTATGCTGCCCCACAGGCTTCTACCCGACCACTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGAGCAGACAGACCCGAGCCCTCAAGGAG
ESTD- CB25	146 A G ---	---	---	GTTTCTTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCTCTTTCTCTCTATCTTCCCGCTC TCTGCTCTGAACCCAGGCGCATGGAGAAATCCAGGACACAGGGGCTGAGGAGGCCAGAGCCACCTG TGACAGGTGAGCTACATGCTCTGTTCTTGTCAACAGAGTCTTACCAGCAAGGGTCTGTCTGCC ACCATCTCTATGAGATCTGTAGGGAAGGCCAACCCTGTATGCCGTG
ESTD- CB27	125 C T ---	---	---	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGGCTGGTGGCATTTACAGGAGTGCTGTGGAGTTCTGCTCATCACTGAC/TTATCTTC TGATTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTTCTCTCCACCCCAATGCT GCTTCTCCTGTTTCATCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T ---	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA/TTATGTA TTTCTTAAACAATAAAGTTGAAGTCCAAAATTACTCTTGATCCATGGACTGCAGAAATAAATGTTA TTTTAGCTGTGAGAAAACAATACTAATCTTGACATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGA TTGCCAATAAGCAGTAATATTTGAGAGGAATCTGTTTCAATGCAGTAG
ESTD- CYP2D6	61 A G ---	---	---	CAGGCCAGCTGGTGGTGGTCAACATCCCGGACAGAACAGGTGAGCCACCACCTATGCAAGJCA GGTCTCATCATGAAGCTGCTCTCAGGGTTCCCTTGGCTGAGCAGGGCGGAGAGCATACTCGG
ESTD- D11S1873	40 A C ---	---	---	AAAAAACAATTTAACACCTTTTCAATCATATAGACCATA/CA/ATTTCCATTTTTCACATAAGTCA GTTTGAAGCTGAGTTTCCAATTACTTGAATCTAAATGTCAATACTGATTAATGAAGTTCAACAG ACAACCTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---	---	---	CATCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGAAAGGCTCCTCTGGGGCGGTG GGGTGTGGCTATGTGGTGTCTGTGTAG/CTGGGGGCTTGGTTTCAGTTGCACATTTGCGTT ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCCTC

-181-

ESTD- D17S33a	75 C T ---	---	CATCCCAAGCCCATCTCTTAGCCACTGGCATTTTTCGCCGCTCTGACAGATACACTCAGGGCCGT CATGCTGCTACACATOCAGGGGGCCCTACCCCTTTGTAGTCCATGGAAAGGCTCTCTGGGGCG GTGGGGTTGTGTGGCTATGTGTGGTCTTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACCTATTGGGTT ATTGCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCTGGCGAACATGGCGAAATCACATCTCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGAGGCTGAGCGAGGAGAAATTGCTTGAACCCJA /JGGAGGCGAGAGCTTGCACTGAGCCCAAGATCACACCCTGCACCTACAGCCTGGGTGACACAGTGGA GACTCTGTCTCAA
ESTD- D3S11	44 G ---	---	AACTGATTAGAACCTGAAATACATATTTATCTGAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCAATTAATAATCCAAATAAGTACACTGTAAATAAGAAATTTAACAGAAATATCATTTGT TTATTCAAACTATTTATCACTATTTTATTTGTTAGGCCATACTAAATCTAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATTAATTGCTGATGTTTGTGATGTTTCCJAGJGGAGCCTTGATGTCAATCTGTATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAAGCTCTACAGCCCTGTTGTTTATTAAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCG TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCTAGAAAGCCAGAGTCATCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTTATTTGGAAGGATGCGCTGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCG TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCTAGAAAGCCAGAGTCATCTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTTATTTGGAAGGATGCGCGTATGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJAGJGTCTCTACATCATCTTTCACAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGGACACCGAGGGCTCCAGGCTGGGGCTTGCACGTGTGGCTCAAGCAGCTCTCGGGCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGAGTGGGAGGGAGACA GAATGCTGATTACJCTGTGTGGAGAACCAAGAACTTCTGGCTGTGGGTAGGGGACGCTGCTTCCAAG ACCTCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAT
ESTD-DMa	66 C G ---	---	GTGGGGACACCGAGGGCTCCAGGCTGGGGCTTGCACGTGTGGCTCAAGCAGCTCTCGGGCTCCACJ GJTTCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGAGTGGGAGGGAGAGA CAGAATGCTGATTATCTGTGTGGAGAACCAAGAACTTCTGGCTGTGGGTAGGGGACGCTGCTTCCAAGA CCTCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAT

ESTD- DRD1	154 C T ---			TCCCAGCCCTATCGGTGCATATTGGACTATGACACTGACGCTCTCTCTGGAGAAGATCCAAOCCATCAC ACAAACGGTCAGCACCCAACTGAACCTGCAGATGAATCCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGCTCTCGCTATTAGAACTAAGGTAC
ESTD- DRD2	144 C ---			TCTGCTTTGGTGCAGGAGGCTGCCGGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCCGGTACAGCCCATCCACCAGCCACCAAGCTGACTCTCCCGGACCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCGCCCAACCAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---			AAGACGATGCCAGGATGAGCGGCAGTAGGAGAGGECATAGTAGGCATGTGGCGGGCTGGCTGG CAGCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTGAGGTGGCTTACTCAGCTGGCTCAGAGATGCC ATAGCCAGAGGAGGTGCGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERB2	93 C T ---			TCTTTACAGGATCCGCATCTGCGCTGGTTGGGCATCGCTCGCTAGGTGTGCGGCTCCACCAGCTGG GGTGAGGGGGTGGGTGAGTGCAGTGCCTTGGGGGCGGTGCAGACCCACGCGGCTGGGAGGACTTCA CCCCGCTCACCTCCGTTTCTGACAGAGTCTCCGATCGTGTACT
ESTD- ETS2	43 A G ---			ACTCACAGTGTCTTTAAGTGAATGTGCGAGAAAGAGGCACCA/GGGAAGCCGCTCCTGGCGCCTG GCAGTCGGTGGGACGGGATGGTTCTGGCTGTGTGAGATCTCAAGGAGCGAGCATGTGTTGGACACA CACAGACTATTTTAGATTTCTTTTGCTTTTGCAACGAGAACAGCAATGCAAAACTCTTTTGAG AGGTTAGGAGGGTGGGAAGGAACAACCATGTCTTTTCAAGATTAGTTG
ESTD-F9	111 A G ---			AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTATAGTTATGCCCA TGCTCCATTTGAGTTAATTTGTGTAAAGTATGATGTTTAA/GTCAAACTTCATTTTTTTTTCC ATAGGTATGTCCAAITTTACAGACAAITTTGTTAAACAAAAAC
EST68787 5	144 A ---			CTTCTATGGGATTTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCAGCTCATGACAATTTGAAGCTGACAATTACACAAGAAAGAAATAAAATTCACAGTCAA AGAAATCAAGCACTTTTCGAACATTTGAAGTTGTTTTTGAACCTTGGTGTACACCTTTAATACAACCTAG CAGACGGAACTGAACCTCAGGGTAAGAAAT
ESTD- GCDH	200 C G ---			CGCAGACCGGTGAGTGTGGGTGGGAGTGTGGAGGGAAGGAGGGAAC/TGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGAACCTCTGTGTCGACCGTGTGTTCTGCTGCCCTGTTTCACTGTCTGTGCTGCCGAGTCT GIGACTCTGTCCCGAAATTCGAGAGCT
ESTD-GCK	88 A G ---			GTTTTATGCATGGCAGCTCTAATGACAGGATGGTACGCCCTGTGAGGCCACTCTGTGTCACCATGAC AACCACAGGCCCTCTCAGGA/GTACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCGAGCGGCGCTGAGCCCAAGGAGGCTAGGATGTGAGAGACACAGTCT ACCTGCAGCCTAATTACTCAAAGCTGTCCCGGAGTACAG

[illegible]

EST45311	151	C T	---			GCCCTCCTCTTCCAAATCTGTCCCTATAGTTTTCTCTATTAAAGTGAACATACATGCATCTCTTTAGTGGATAGTGCACACAACACAGCCATTATGGGGAAGGATCCAGTGTGTGGCCCATATTGTAACA CATTTTCTGCAAAATC/TACCTCTTTTCATTTAACAGCCCTTATTCATAGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCAATTTGTTGAAT
EST65258	80	A G	---			TGCCCATCACGGCGCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTTCQ/G CCCTCAAAATGACAGCCATGGCGCGGGTCTTCTGGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGGCACAGTCTTTGTCATGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGCGGTTTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216	26	A T	---			ATGCAGGATGAAGGTGGACAGGGAGG ATGAGGGCCAACTGTCTATCCAGGGCCTGCAGATGTCG CTGGACTATGGGTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	149	G T	---			ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTTAGCATTTGTTTAGCATTAACCTAA TTTTTTCTCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTCTCTC G TAAAGTGCCAGTATCCAGAGTTTGGTTTGAAGTGAATGCAATGCCGTGTGAA AAAGAACTGAATACCTAAGATTTCTGTCTGGGGTTTTTGGTGCAATGCA
ESTD- KRT10b	183	C T	---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGTTTTTCCATTAACCACATATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAG C T TGCTTTTAAATAGT CTGTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133	A G	---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGTTTTTCCATTAACCACATATTACTTCTA A G GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCTTTTAAATAGTCT TCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231	C T	---			ACCCTCACCCCTCCCTTAGCC C TGTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAGAGAGGGGCCAGATGTTAAGTACAAAAGTGAGGGCCCATAG GCTGCCATCTCTCCCGTCTCAGGTTTACC A C T GTCAACATTGACACA
ESTD- KRT8a	21	C T	---			ACCCTCACCCCTCCCTTAGCC C TGTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGTCAAGACTAAGAGAGGGGCCAGATGTTAAGTACAAAAGTGAGGGCCCAT GGCTGCCATCTCTCCCGTCTCAGGTTTACCAGTCAACATTGACACA
EST75099	82	C T	---			CACCTGTGTGTCTAGATCTCTCAGTGGCCGCTCTACTGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA C T GGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCACC CCTTCTCCTGGCGCTCTTGAGGTGTGG

ESTD-LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTTAACCCTGTAACCTGCCTCTGCCATGCAGCATCATAGCCTGT AAAATAAAATTTCCAATATGTAGTGTGTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCGAGGAGGGCTCCCTACCCACAG
EST35879 9	142 A C ---	---	GAGATCGGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG GAACTCCGGGCAATCCTGACACGTGTGCACCCAGCTGTACCCAAATTAGTGAACATGGCTTCGAG AGAGTTGACJACAGATTCCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA A
ESTD-LMP2	35 C G ---	---	TACACACTTTCCTTACCAATTCACCTGAAACGACTCAGCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTTCAGCTCTGGCTGTCTGCTGCTGCTGCA AGGGTTTGCTTAATCTCAATCAATGTCTCTTCACTCTTTAGCTGTGGGGTTTGTGTTG TTCTCTGTTTTGCTTAGTATCTGACTACTTTTAAATATAAAAGAGATGTATCTAAACAAATAG AGATTGTTATCAGAAGTTCACAACATTTATTAATAATTTTTCACCTG
ESTD-MOC	45 C T ---	---	TTGTCAGGAGTGTGCTGATGCTGCCTCCAGCTCTGCTCCCTAGCTCTGAACTTCAGGACAACGTGC AG
ESTD-METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA TCTCAGGAAGTCTGCTGCTTCCCAAGGGTTGGTCTAAGTTGCTGATTACCTCTGGATTTTCTGACG ATCTTCACTGCTAGAGCATCTGCTGCTGTTTTCATG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAACTGATACCAGATCCACAGACTGATATGGCTGGT AACATGGACTGTATATTTGTACAAAAAAGTTTTATTTCTAAAAAAGAAAAAAGAGAAA AAATTTAAGGGTACTTATATCCACACTGCACACTGCCTAGGCCAAACGCTTATTGTGGT AGGATCAGCCCTCATTTGTGCTTTGTGAACCTTTGTAGGGACGAGAAAGATCATTTGAAATCT GAGAAAACCTCTTTAAACCTCACCTTTGTGGGGTTTTGGAGAAAGTTATCA
ESTD-NFKB1	107 A G ---	---	TGTCCTTAGGCCAGCCCTGCTTGTCTCCCTGGCTGTATCTTQAGTACTGCAAGAGAACACA GACAT
ESTD-NPPA	45 A G ---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATAITCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTTATGTAGGGTGATATGGACTCTTTTGTGATTATATATAGCAATTTGAGGG ACAAACCATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTAACTTGGCAATAGCATTTG CTTATCCCTGTGTTTTTAAATAAAAT
ESTD-NRAS	202 C T ---	---	GCCACCACCCACCCACACACCTCCAACTCAGCCAGACAAGGTTGTGACACAAGAGAGCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGGAGGTGACCCGTGTATCATCGGAGCGCCGGG CACATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGCCCAAGTCTTAGACAGACAAACCC TAGACAATCAGTGGCTGGCT
ESTD-PAI1	100 A G ---	---	

ESTD-PAR	120 A	---	---	CTCTTCAGGAACCACGAGTCTTCTTACCAACACGAGCTTATTGCTGTCCGAGAGGTACAAACCCGCTAGA ACTTCTTCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCOCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTTCACTTTCTGTGTTCTAGAACGTTTCTTAG GACTGGCAGTTTAAGCTTTCAGTTAGGCTTCTGTATACCATGCC	
ESTD- Per/RDS	74 A	G	---	ACCTACAGACGTCGCTGGATGGTGTGTCCAACCCGAGGAATCTGAGAGCGAGAGCAGGGCTGGCTG CTGGAGA/GAGCGGTGCCGAGACCTGGAAGGCOCT	
EST68308	5	29 C	---	GGAAAGAGATTTAAGAAAGCTTGATTGGAC/TJAATCTGGTCTTTGAGTGTGGAAGAGTTTCATGTC TCTGCCTGAGTTACAACAGAAATCCTTTAGTACAGCAGTAATAGATATATTCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTATTTTTTA	
EST54045	6	39 A	G	---	GGATATTAAAAATATTTAAAAACCTCCATTTTGCTT/GJTCCTTTTAGTGAAGATGATACCTGCG AAAAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTTCTTACAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTTGCCTTGGAAITGGATTTTAAATGTGACTTTATCAT
ESTD- PXMP1	88 A	G	---	---	ATGAACATGGTCTTTAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAA/A/GJAGCGAGCTGTGTGGACAAGGTGTTTTCTCAAGGCTCATAC AGATTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAAGTCTTATGAAATTATAATCTT
ESTD-RDS	127 A	---	---	---	CCCGAGGAATCTGAGAGCGAGCGAGGGCTGCTGTGGAGAAGAGCGTCCGCGAGACCTGGAAGG CCTTCTGGAGAGTGTGAAGAGCTGGCAAGGCAACAGGTGGAAAGCCAGGCGCAGACGCGAGG CCAGGCCCAGAGGCTGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACT CCAAGAAACGTGGATCTCCCCCTCATCCAACCTCCGAAAGTCTGAA
ESTD- s14544	94 G	T	---	---	TTGGGAAGTTAGAGCCTATATTAATTAACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTG/TJCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
EST52908	0	45 A	C	---	ATCACAGGTCTGTGGTCTCTGGCCATCATTTCCCTGGGAGAGATGG/A/C/JGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST19590	55 C	T	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGTCTJGGCTCAG GATGCCGGAAAAATGAC
EST76136	39 C	T	---	---	TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACCC/C/TJGGTGCATACCTTTATCTATAGCCTT CCCCTAGGTCTT
ESTD- SPTB	176 C	T	---	---	TGAACACCCCTGTGTCCGGAGCCAGGTGTGTTTCTCCTGGGAGCCTGAGGAGTTTGTGTCTGTGTG CAGTCCCCCGCCACCTGCTGTGTGAGCCTGGACATACACCTTCACCTCTTGGCCCGGAGAAGAC ATTTACCCACCTGGCCATGTCCCTGGCCCTGTTGTGCACA/C/TJCTCTGTGAAGACCCCAACCCCTGC CTCCCCACCCAGCCAGTTTCTAGCAAGGGCAGGAC

ESTD-TAT	224 C ---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGGTACCAATTTTCATCAGGGCCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTTTACAACCTTTCTCCAGTATGGATGGATTATGATGGGGGG GAGAAGCAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THR	125 A C ---	---	TGGGCCCTTCTCCGGCAGGTGAGTCTTACTTGGCTGTGATTTCCAAGAGAAAGAGTCCCAAG CACAGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATCJACJCTTCAT CCACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGATTCTTGTCCACCACCAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCAGTATCCCCAA GCAGTGCATCCATTGACACATAAATATGCATCCAGACAAGAGGTCATAAATATTGATGTCGTTAA CATGGGTGTGATCCATTTTCATTTGGCCATAGGTCCCTATGGGGATGACA
ESTD-TYR	122 G T ---	---	AGTAGTGGATGAAGCTAACAGCCTCTCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACA AACCACCTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTCACCTTATTACCTTCTTCT AATACAAGCATATGTTAGTACJATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C ---	---	AGTAGTGGATGAAGCTAACAGCCTCTCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACA AACCACCTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTCACCTTATTACCTTCTTCT AATACAAGCATATGTTAGTACJATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C ---	---	TTCCCAAGGCCTCAATACAAGTCTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCAJCTCAGACTGAGAACCCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 C T ---	---	TTCCCAAGGCCTCAATACAAGTCTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCAJCTCAGACTGAGAACCCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T ---	---	TTCCCAAGGCCTCAATACAAGTCTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACJAGTGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCACAGAGACAGGAACACC GTGACTCTGAGATGTCAJCTCAGACTGAGAACCCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G ---	---	ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---			CTCTGGATGGTTACAGGTGGCAGGCACAAAGCCAGTCCATCCTGTAGTCATCATAGTTGTGGCTCC CAAGTTGCTCTCTCTACTGAGAACAGGACAGCCACAGTGTCGCGGGATGCGCGGGAGTTTC TGGTTGCGCCACGGCTGTGCTCTGTGTGAACGGTAGCCTTTCGGTTGCGATGCCTAAACCTTTGT TTCTTGCCCAAGAGGGCGGGGTGCCATGCTGAGTGTAGATGCGGCC
ESTD-VWF 6	36 G ---			AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCTTTGG TCCCTAGAGTCTG
EST71770 6	189 C G ---			AGCACCACTCTCACGTCAGCCTCAGCACACAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCTCATGAAGAGCAGAGAGATTATTTTATCTGAACTCCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAG[C/G]JGTGGTGGGA AGGAGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGCCCATCCAAGG
ESTD- TNFαb	152 A G ---			TTCTGCATCCTGTCTGGAAGTTAGAAGAAACAGACACAGCTGTCCCAAAAGAAATGGAGG CAATAGGTTTGGAGGCGATGAGGACGGGTTTACGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAGACCCCTC[G/G]AAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTTGATG CTTGTGTCCCAACTTCCAAATCCCGCCCGCGATGG
ESTD- TNFαa	88 A ---			TTCTGCATCCTGTCTGGAAGTTAGAAGAAACAGACACAGACCTGTCCCAAAAGAAATGGAGG CAATAGGTTTGGAGGCGATGAGGACGGGTTTACGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAGACCCCTCAGAAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGTCCCAACTTCCAAATCCCGCCCGCGATGG
EST52418 6	113 A G ---			CAAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCAGTCACCTTTGGTGGCTACAAGATGTG GGGAGTGGCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACT[G/G]AAGTGAAAACGTGTGAGTG TGG
EST13586 3	89 A G ---			CCCACTCTATTTGCCAGCCCAAGGACAGAGCTGATCCTTGAACCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC[G/G]GGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCTGCTGCTGCTGCC CCGGTCACTC
EST51976 7	123 A T ---			AGGCAGAACTGGGCCCCCATGCGGGGACGTGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAG[G/T]CTCTCTC CTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGGAGCAGCAGGAGCAGGAGGAGGTGCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST11458 6	140 A G ---			CCACTTTGGTAGTGCAGTGTGACTCATCCACAATGATTCTCCAGTGTCTATCTTCTCGAGTTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTGTCAGGAGATGATTTACCATTTTCCACAGTGGT CCC[G/T]TAAAACATCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTG TCCGAGGAGGGATGAGAAAGTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ---			AGACCTCAGTTTCTCTGTAAAGGGAAGTTTGTCTTGGATCTCCATGGGCCAGC/C/TAGCA CTGGTGCCTGTGAGTCTGTATCAGGTAGAGATGGGACCAGGTGGAGAGAAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAAGAGCTGGGAAATGTGG
EST39852 8	106 C G ---			CGGTCTTCTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTAC/GJGGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAGGCCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCTCCACAGGCTGTAT AATACAGCCCT
EST62448 0	112 A G ---			ACCTGGTGTCTGCTGTGGGTGAACCTGGTCTCTTGGCATTGCCGCCCTCTCTGGGGCCCGTGG TCTCTGTGTCTGTGGGTAGTCTCTGGAGTCAACGGTGTCTCTTAC/GJGTAAGCTGGTCTGATGGCA ACCTGGGAACGATGGTCCCGCAGGTCCGATGGTCAACCCGGACACAAGGGAGAGCGCGGTTAOCOC TGGCAATAT
EST36027 2	120 A C ---			AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACCTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGG/C/CAACCTGAAAA AGGCTGTCACTTACAGGGCTCTAATGATGTTGAACCTTGTCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTTGTAGATGGCTGCTCTAAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112 A G ---			AGAAATGTATATAGTCTCAAACCTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTCTGCTCACTTTC/AGJGGGTGTTCAAGGTGAAAA GGTGAACAGGTCOCGCTGCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAACTACTGCCT TTGGTCAGCCTATTGAGCTGTAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T ---			TGAGAGAACACCTAGTCTCCATCCTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTGCTGGACCTGGAAACA/C/TJGGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTGACCAACACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---			GCCGCAATGCCCGGGAGTTTCTCCAATGTGTGGAGAAGGCCCTTAGAAGACATGTTTGATGCCCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGCAGATGAAAAGCTACCATCACTTCTCATCATGAAAAAC TGGAGGCCCGGCAT/AGJGTGCTCATGCCGTGTAATCCAGCATTTTGAGAGGCTGAGCGGGTGGAT CACTTGAGGTGAGGAGTTTGAGACCAACCTGGCCAACAT
EST12274 0	135 A G ---			CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAGTGTAT TACATAAAGAAGTCAAGTGTGTTTACTCTCTCATGACCAAAATATCTTCCCTCTTAGGATGAGGTG A/GTAGTAATGACCGATGGGTGAGAACTGTTCTGTCACTGAGGATGAGGATATACTGTGAAGA TAAATTCAAGCCACAGAGCTTGCCAGATC
EST76807	91 G ---			ATGCTAAGGGGATCGGACATGAAGGACCCCTGTAGCCGATGTCTCTATCTCCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCACTGCCCT GCTGCCATGTGGACTGGTGTCAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---	---	TTCACTTTGTGGATTGTTCTTTTGTCTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGTCTTGGCTGCTGTCTTGTGGATATTTGAAAGAGATCTTTTGCAGTCCCAATGTCCCTAGA GAGTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGGGCCCTTAGATTTAAGTCTTTAATCCATT TTGATTGATTTCIGTA
ESTD-FYR1	109 A G ---	---	CTTCGTACGGGAGGTCACGTCTCCGCTCTTTCATGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTATGACACGACGACACTTGTCTACTATAGAG/GGGGAGCTGTGTGCACTCATGCC CGCTCCCTCTGGAGCTGGAGCCACTGAGAACTAGCTGGAGTGGAGCCACCTGGCTGGGGGACGCC ACTCGAGTCCGGCATGTCACTACCGGCGAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---	---	AAGACTACGTGAATGTTACATGTGCTTAAAGCTCCCTTCTCTTACTCTGCTGCAGGATGTG CG/G/GJCGTGTGCTGGAGTAGCCCCGACTCTTGTACGGTGGCATCTGAGACCAGTGAGAAACGCC CTTCATGTGTGCTTACCAGGCTGCAA
ESTD-F2 EST4438 7	100 C --- 62 C T ---	---	GATAAGTACACTGAGGCCCCAGGAGTTATTGCCTAGTAGCCCCAACTGTGCATGCACGCTTAACTCT GCACCAATGGCTCCAGGCCCGTAGGGAACTGGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGGCCGTGCTGGGTCCCAACAGAGGAGGCCCTGGAGGAGACAGGAGATGGGC TGATGAG
ESTD-PBDA	103 A G ---	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA/C/TJG TCCTGCTCCGACCTAAGCGGAGCAGCTCAAGAGCGAGCGAGGTGGG
EST12839 3	122 A G ---	---	CCTTCTCATGCCAGATGGAATTCAGTCCCTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAA/GJ/CTCTACCCGCGAGCTTGTCTGCATACAG ACGGACAGTGTGGTGCAACATTGAAGCCTCGTACC
ESTD-CTLA-4	48 A G ---	---	TGCAAAACACACAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAG/GJ/CTCAAGTCCA AGGCCATTGGCTATCTCAACACTGGTGAATGATTACTTGAAGGGAACCTTGAATGTTATTCAAC TGGATTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
ESTD-ACE	96 C T ---	---	ATGGCTTGCCCTTGGATTTCAGCGGCACAGGCTCAGCTGAACCTGGCT/GJCCAGGAOCTGGCCCTG CACTCTCCTGTTTTTCTTCTTCTCATCCCTGTCTTGTCAAGCAATGCACGTGGCCAGCCTGTGT GGTACTGGCCAGCAGCGGAGGCATCGCCAGCTTGTGTGTGATGATCATCTCCAGGCAAGGCCAC
EST54419 8	88 A G ---	---	GATCAAGCAGTGCACACGGGTACGATGGACAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACTGCAGTACAAGATCTGC/CJ/TGTCTCCCTGCTGGGGGGCCAAACCCGGCTTCCA TGAGGCCATTGGGGACGTGCTGGCGCTCTCGGTCTCCACTCTGAACATCTGCACAAATCGGCCTGC CTTCTGCCCTAATTGAATGATATTGTTGCTGTGGGACCTGAGCACTTTTATGGCACAAATGATCACTA TTTTCTGACCCCTACTAC/GJATCCTGGGAGATGATTTGGGTTAGCGTGGTGTGTTGTGCTA CTATAGTCCAAGTGAA

ESTD-PS-1	99 A G ---	---	GGGGAGTAAACTTGGATTGGAGATTTCATTTCTACAGTGTCTGGTTGGTTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACAAACCATAGCCTAGTTCGTAGCCATATTAATTGGTTGTGCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	GGCTGCCAGGGTTCCGTGGAGCGGCGCCTAGCGGGGCGCCTGCTGGGCTGGCGGTGCTGGCAAC GTGGAGGCAACCTGCTGGTTCATCGTGCCCATCGCCCTGGACTCGAGACTCCAGAACCATGACCAA CGTGTCTGTGACTTCGCTGGCGGCAGCGACCTGTGTGATGGACTCTGTGTGTGCGCGCGGCGGCGCA CCTTGGGCGC
WI-567b	48 A G ---	---	TCTCACACTGACCCCTTACCTTCATCCTCACCTCTGCTGCTTGGTTCTGAGCCCTCATCTCTTTA CAGGATCCGCCACAGCATCCCACTGATCTGGCCTTAGGCTTCTTCTCCAATCCATTCTTCAAAAG GCTGCCACTGTGATCTTCCAAAGTGATTCGTGCTGCTACCATCTGCTTCAAGCC
WI-801c	58 G T ---	---	ATGGAACATTTCTCCATAATGAATGAGGTTCTCAATCCATTACACATCCCTTTCTGTTAGATGG TATTGGAGAGTAGACAGAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACACAGAGAGTTAA CATTCTGCCACCCCTC
WI-801b	58 G T ---	---	ATGGAACATTTCTCCATAATGAATGAGGTTCTCAATCCATTACACATCCCTTTCTGTTAGATGG TATTGGAGAGTAGACAGAGAGAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACACAGAGAGTTAA CATTCTGCCACCCCTC
WI-1098b	76 A G ---	---	GAAATTCACCTATACAAGAACTATTTCTCTAATTAATTACATTAGTCTCATTTCTGAAATATTAT TTTTTACAAGTACCCCTTTGATTAATTTTGAATTCATTGTAAACGAGAGATTACAATATCAGTAACGC TGTTCAATTGATAGTGTATCACAAATGTCTAAATACTTTTGGGTCAACATCAAAATTAGAAAGAA CTTACAAAGTTTATTTGCTTTATGGTTA
WI-2529	71 C T ---	---	AGGAAATGGCTGATACCTCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA/C/TJCTTAACCTGCTGCCCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATTAAGTGAAGAGGTTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACCTTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---	---	TAAGGGCCTGTCTTCCGCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACATATAAGAGAGACCTGTACCTATAGAGTAACTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAGACTTTTACATTTTAGAC AGG/C/GAGCAGAGCAGCAAGGAGAGAAAGGAAGT

WI-2625	98 G A ---	---	---	GGCAGTCTCGCTGTAGTGGTAGACAGCACTGAAGGATGGAGGAAGAGAGAAACAGGCAGAA GCACTGTGGTAGTTAACAAGGCTTATTTAGGA[G/A]CAAAATTGATGATCTCCCTGAGGACTCGCAG AAATTACCAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATTCACCTTGCAGGAGGAAAGCCA GCCAGCAAAG
WI-2924	54 G A TAGG	TGACCTTCCTA GTCTCTCTTA	GCCTAAGTGT AATCACAGGG	TCTGTTGTCATATTCCTCTTTGACTCTGACCTTCCTAGTCTTCTCTTATAGG[G/A]ACCCTGTGATT ACACTAGGGCTACCTGGATTATTTAGAACAAATC CCATTGTTGAGTTGGTGGGTCACTTGTCAATCCCTCGCACTCAACAAGTGGCTTGTCTCAGTGC CTTT[G/Γ]CAAGACCTTCCTCAACAAGAATGCTTTCCATGCTCCGTTCTTTGAAAATTCGACT TTATCTGAAAAACTCAGCTGCAGTGTATCTCGGTATAAAGCCACTCCTG
WI-2939	72 G T GTGCCITT	GGCTTGTCTCA	CTTGTGAGGG AAGGTCTTG	CTTGCTACCATGCATTTACAGCATACAACCTCAGTGAATGCCGTAAACCCCATTTATAAAACAT CTTGCCATCGAAGGGTTATGCCGACAGCAG[G/A]CCACACAAGGCACTACTTGAAGTGACTTGGA GAATAAGATTTTGGATGGATGAAGCAGAGAGGAGATGCTAAAAGTGA GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGATAGTTGGTAGGCCCTGTTTGGA GATTGCAGAGAAGGAAGCAATTTAGCCCTAGGGA[G/Γ]TAGAAAATGTTGGTGACATCAGGGCT ACACACTTTCTGTATGCTCTTCATCAA[G/Γ]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATGTCTTGGCTCCCC
WI-3203	99 G A AGACGAG	GGTTATGCCGC AGCATTTTA	TCAAGTATTGC CTTGTGTGG	ACACACTTTCTGTATGCTCTTCATCAA[G/Γ]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATGTCTTGGCTCCCC
WI-3473	101 A G GCCCTAGGGA	GTAGTCACATT AGGTATTTTCC	GAGAGATATTT TTCAGAGGCAT TTT	AGTGTCCATCTTCAGGGTTAACTCTGGATCTGGCTGCAGAGTAGGAAAGAAAGATGGGGTGAGT AGTCACATTAGGTATTTCCAAATA[Γ]AAAATGCTCTGAAAAATATCTCTCCCATGTCCCTGTCT TAAATAACATTTTCCC
WI-1796b	29 A G ---	---	---	GCTGAGCTTTGTGGCAGAGCCAGGACAATTCAGCTGCCGGATTTTAATAGATTCTGCAGCACTGCAA CAGGAACCAAAAATCAGTC[Γ]TGGTAACTGAGAGTGGTTTTCACACCCAAA
WI-1796	29 A G ---	---	---	GTGTGCCCTGTAGCAGACACAGAAGGCA[G/Γ]AGAGGAAAAAGCCTTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-4360	93 C T AAATAA	---	---	CTTGAGTATCGTGGATTTTGGTATACAGAAAAATGGAGAGCTGGAACTAATCCCCCATATACCA AGGGACAAAATTGTATCTGTTCTACAAATTACAGTAGGAGACATTATGTTCCATGACAATGGTAAT TTTTAA[Γ]TGACAGTTTTTAATTGAGTGAATACCATAAAAAATAATAAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGCCTATAAATAGC
WI-1959b	87 C T ---	---	---	
WI-1973b	28 A G ---	---	---	
WI-1980b	140 C T ---	---	---	

WI-2015b	190 A G ---				TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCACAAAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTGTCTTTTCCAACT[A/G]CATATACTT CTAATACCATAGAG
WI-754b	49 C T ---				GAAGGCACAGGGAGAGATGCTGTCTATCTACAGCCAGGGAGAGAGAGCC[C/T]ACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAAAATTTGTATTACTTTAGA
WI-754	22 T C ---				GAAGGCACAGGGAGAGATGGCT[C/G]TCATCTACCAGCCAGGGAGAGAGAGCCACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAAAATTTGTATTACTTTAGA
WIR-1b	56 A G ---				AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAAACTCTGTATGTATGTCATCC[A/G]TGCCTG GAGGGTGAATGCTCTCTGAGGACATGGGAGCTTCATGTTTGAGCCCTCCCTG
WIR-1	56 A G ---				AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAAACTCTGTATGTATGTCATCC[A/G]TGCCTG GAGGGTGAATGCTCTCTGAGGACATGGGAGCTTCATGTTTGAGCCCTCCCTG
WIR-3b	72 A G ---				TAATTTTAAATGGGGCCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT[A/G]TCTAAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTGAATGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---				TAATTTTAAATGGGGCCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GA[A/T]GTATCTAAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTGAATGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---				GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATCCCTGCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209 C ---				CGGGACAGAGACAGAGAGAGAGTCTGAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196 C ---				CGGGACAGAGACAGAGAGAGTCTGAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194 C ---				CGGGACAGAGACAGAGAGAGTCTGAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGATGAGAAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5c	177 C	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGATGAGAAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5b	159 A	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGATGAGAAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTT AGGTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACAC AGGTTTACGTCCAG
WIR-5a	37 A	G	---	TAACCTGAAACTTTGTCTCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGTCTTGGGGTTGGGCAG
WIR-6	63 A	C	---	TTCTGACTATTTC/TAAAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12 C	T	---	GGCGTCTATGACTATCCTGGTCATTGATTGACTAATGATTCCTG[C/T]GCCCTTG
WIR-8	46 C	T	---	AAACAGAAAAATAGAGTTTAAAGGATGGAACCTAAAGTTGTCAGAAGAGGTATGA[C/G]CTGAAG AAAGAAATTACTCTCTTTTGACCAATAAATACAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAC
WIR-2	56 C	G	---	TGTCTTGCTTATGCCCTGCTCTTTCGCTTGGCAGGATGCTGTCATTAGTATTTTACAAGAAGTA GCTTCAGAGGTAACCTTAACAGAGT[G/A]TCAGATCTATCTTGTCATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTACTGACATTAGCAGCATCTTTAACACAGCCGTTGTTCAAAT GTACAGTGGTCTTTTTCAGAGTTGGACTTCTAGACTCACTGTTCTCACTC
WI-7069	93 G	A	---	GGTCATTCTCTTTTATCTGTCAGGCGCCAGCTGACTTATCTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A	T	---	CACACTGTTACACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAAGTA TTCATGAAGAATGCATAATCTCTGAAAAATTATGAAAACATCCCT
WI-18612	37 A	G	TGC	TTGATTGCTG CTTGCAAT

WI-18517	87	C T	CAGGAATCAG CAGCCTGA	TGTTTGACAA GTGCAACA	TTAAAAATCACTAGGGCTCACCCCTCAACACCCCTCCATTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA/C/TJTGTCACCTTGTCCTCAACACACACTGACTGC
WI-18668	76	C T	GGGAAAAAC TAGGCAAAA	GCTAAATTAAA CTGCACTTTT GC	CGATTGACAACTTTTATTTTCAACTAGGTAAACAGTCCAAAATCAGTGTAGATTGGCGAAAACT AGGCAAAA/C/TJAGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75	T C A	GCCTGCACTCT AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT/CJGCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A C	GGTTCTCGA GGGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTGTGCGAGCAACACCAAGGGCAGGTGGGCTTGAAGGAGCC CTTGAGGAAACACAGGCTTCTCGAGGGGTAC/CJCCAGCAGGGCTCAGCTTAAAGTCG
WI-18673	29	A G	---	---	TGTGGGCAACCTTGTTTAAATTTGCAAA/CJGJACTTAAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAAACATATGAATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAGCGCATACAAGGAAG
WI-18640	121	T C	GTCGTGGGGTG GGG	GCAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTTGGAGGTTAATTCCTATAGGATATGAAGGATTGACCAACGATTGAGATT GTGTTCTCACGGAGGGCTCGGGCCAAGGTGCTGGGGGGGTGAGAG/CJGTGTCTCTCTTC AGTGGTATTGGGGAC
WI-18533b	91	T C	---	---	GGGGAGAGGAGGTAGATGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCTCTTTATTT TATATTTTCATTTTTCATCCTAAT/CJTTACTGAAGCCATTTCTTTGGTTAACTTAGA
WI-18533a	59	T G	---	---	GGGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCTT/GJCTTTA TTTTATATTTTCATTTTTCATCTCTAATTTACTGAAGCCATTTCTTTGGTTAACTTAGA
D11734	83	A C	TCATCTGATAC CTTGTTGAGAT CTT	AACCAGGATA AGGCTACAAC ATT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCATCTGATA CCTTGTTGAGATT/CJAAATAGTTGTAGCCTTATCCTGGTTTTACAGATGTGAAACTTT
D49493	159	A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGGC	CAGGACTTGTGGTCAGCTGCAGACACAGAGCAGCTCATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATAGGGGTCTTTCATTGCTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATT/TJGCCCTGGCCTGAAAGTGGCCCATCATTCATACCCACTGTT CT
EST10030 7	98	T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTTCATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCTT/CJTCATCCATACCACTGCTGATTG
EST10052 2	24	G A	GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTCTGGAGGCTG/GJAGAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTGCATAACCTGGTGGGAAGTGCATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGAA A

EST10605 2	118 C G ---			CTTGGTAAATCACAGTTCTGTATTATACAAAAACCTTTGTTTCTCTGACAAAACGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCCCATGTTC/GJTTGTGAGACTTAA AAAAAAGAAAAAGATCCC
EST11048 0	61 T G	CTCTCAAGTAG ATAAGAGGCA TAATCT	GCTAAATTTTC AGAAAGAATT TTGTTT	CATGTGTCATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT/GJAA ACAAATCTTTCTGAAAAATTTAGCTTATGAACCTCATTAACACTGCAAAACCAGAGAAGGAGCAC TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAAGTCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG/GJTTGGAAATGAAGGCAATATCAGATAAA TTTGATGGAGAAATCCGAGGCTGCCAGCATCCACCAGTAGATTTCTTTGGACGAAGAAATCCT TCTGTGGATTACGCTTTACCGCTTTCTCTCATCTGCTGTGTTC/JTTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
EST11349 9	109 C T ---		---	GAATCTGGGTATTAAATAGCGGGTCCACAGGAGCACATAGGAAGAGCATCCAACCTACTTTGGAG CCCTT/GJAGGAGTTTATAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGAGGAAGGAGTGGGAA
WI- 16632a	71 A G TGGAGCCT	CCAACCTACTT	CTAAAACTCC T	CCAGGAATAAAAAAGAAAGTCAAGAGGAAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA/GJGACTATTTCACTGACTATAAGTGAATAAATACATTTGAAGACTTCAGGAGCTCA CTTGCCATTATTTGTGCATGTTGTTCTTAAAGGCTGTGAAAGATAACTTTGGAATGTGGGAAAC ACATAGATCCAGAG/ATATTAAGGGGCTGGAAAAGTAGCCTTAAGAC
EST11772 6	74 A G ---		---	AGAGCAATGGTGCATCTCAATAAGCAGCTCATTTTGATTAC/GJGGTATACATGAAGTAAAAATTC ATGAAGTAAAAATTCATTATACCAAAAAGCCTCCACAGAACTTTCATGCACCCTGAGCTATGTGAAC TGAAAAAGTAACAGTGGGAT
EST11795 3	82 G A ---	CAATAAGCAG CTCATTTTGAT	ACTTCATGAAT TTTACTTCATG TATACC	GCCTAGTAATCCAAAAGGAACATGTTTGATATAATAACACTCAGTACAAAAGTCTGT/GJATCCAGG AAGTGACCAGCCCGACGTGTCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC GTGGAAAAATTTTTATCTGTACGCTTTCC/JATTATATTTATCTGTCTTGATTTCAGCACCC CACCCGATTTGCAGGCGAGTCTTTCTAAACTGTGCCCTGTGAGCTGTTAAAAAGTCTTCT CCCTAGCAAAATGACTTGGAGTTGTGTCCTCAATTACCAAGTTACATACTGTGGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT/GJGGAAACGCACAGCAAAAATTGACGATGCAGCTTTTA CCTTTTITA
WI-16644	42 G A TAC	TTGTATAATA ACACTCAGTA CAAAGTCTGT	GGCTGGTCACT TOCTGGAT	ATCTTGAGGTTTCTGGCCCTGTCAG/GJAGGTGACATCTTTTACTTACCACAGGTGAGAACCTTAT AAAGAACTGTGTAGAAAAGATATCAGGTGAGACTTTTTTAAAGGGCTTCTTATCAGCTCAATAAA
EST12005 9	56 A G CAAAGTCTGT		---	
EST12055 9	32 T C ---		---	
EST12492 1b	95 A G ---		---	
EST12492 4	25 A G ---		---	

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EST12502 2	52 C G ---			ATACTAGGGAGAAACCAAACTGGAGGCAAGTCCACAGTGCACACTTGTCA[C/G]CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAAATGCTCACGGGGAAATGACCAATTTTAAGGGCCATGTG GTCGTCGAGGCAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAAATTAGAATGTATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTACAAA CAGGTGTTTATATCCCAATGACAGTGTGCTGAGAT[C/G]GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTCTCTCTCTCTCATTTATTCATTTGTTCAAAACACTGTCTAGTACCAACAATTGTCCACCGGC[A /G]TTGAGAATACAAATATTGAAGAAGAGTCACTGCCTGCCCTCTGGAANAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGTTCTCCAGGATTCAG[C/A]CTGAGTGTGATGTGATGAGTTCTCATCCATGCTCCACGG GTTCTGGGAGTGACCGGATGGGAATCCATGTGCTTTGCTACTCCATCAGGTCATTGCG
EST12941 8	23 T A ---			TCTCAGCTCCACCTGACCTGCAIT[A/CAACAGCCCAAGTTATTTACCAGAAATTTGTTGCGTTTCA ATGTAGTGTTAGCTTTAATACACTGCACCTGTTTG
EST12949 2a	52 A G A T A C T G T T GGCTTTAATCA TAACCTAATA GGGTCTC			AGGATTTTCATGAGGCTTTAATCATACCTAATAACTGTTAAACAAACACAC[A/G]TCTGTCACCTG CAGAGACCCACAGGACACACATTTCTTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTGTGTTTCTTAATGAAGCATAATAACAGTTAAATCTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTAAATCAGTCTTCTAGGCCACAC[A/CTGGAGCAGAAAGCAGCTTCCCACCCAAG CACCTCTGAAC
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCTTTTAAAAATTTAATCGCTTTATACAATTGACACCAATAAAATGCAC[A/ /G]TATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTCTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTTCTGTGTGTGCGCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTGAGGAAATAAAATTAATGAAATAGTCT GGCCATT[C/G]GACTAACCAAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAACAAACATG
EST13230 6	72 G A A G A C G C ACAGAGA			GCATCATCAGCGGCTTTTACTGAACTTACAACCAACTTGCCGCTCAATATGACGCTCAGATGTGAGAG ACG[C/GA]TCTCTGTACAGGAGCCGCTACTGTCTTCAATCCTTTGTCATGAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C T C T C A G G C C T TGACAAAAGA G			AAAGATATAAAACAACTCCCATCAGTAGCAATACAAGGTTATACATTTTAAACCAGATTTTCTCAGG CCTT[C]TTTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAAACCCCTCTGTATATAACCA

EST13278 2a	51 A G	CTTCCACCGAA CAATATTTTAG	CATATCTTGG GTGGTGAGAA	TTCCGAGAAGCTTTTACAAGCTCCAAACCTTTACCCGAACAATATTTTAGG[A/G]ATTTGAAATAT
EST13282 0	99 A T	CCACACATTTTC AGTCCAAGA	GATGGAATAAT TGAGGAAGGTT	TTCTGTAGTTCTACCAACCCCAAGAAATATGACAGCTTG GCTCAGTAGATGAGCATTGACCAAAATATTTAGATAATACCTGTGGGAAAGTGCTGAATTAAGTCC TGCTGAGAATCCACACATTTTCTGCTCAAGAA[A/T]AACCTTCTCTCAAAATTTTCCATCTCCCATCAGA
EST13290 9	39 A G	CAATTTT TAGA AGTTGGGTTT	AAATCAGCTTCA TGGAATAATTTCA	AGCTCATCTGCAAGCAATTTTGAAGTTTGGGTTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTTCAAGTTACTTAAGACCTAAAGACAAAGTGATATCACATCACATATTTTGT ATGTGTTGGGCTTTTGTG
EST13518 2	45 C G			GAACATCCTCCAGTAGTATTGAGGTTAAATGATTCAGCATT[A/C]ACTTTAAAAATTAACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCTTATAACCTTGATTG
EST13522 8a	66 A G			CAGGTTGGTGATTCTCAACTAGGAGCTATTTGCCCCCATCCCCCAGGAGTCTGGAGAC[A/ G]GTTTGTGTTGTCACAACCTGCGAGAGGTGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C			CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGTTGAGAGCCATTGGTCTAGGAGTAGA AA[T/C]GACACAAAGGAATAAGGGAGAAGGAGGTTGGGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101 C G			AAGATTACGGACCATAGAAGCTGCCCCCGACCCATACACACAAATTTATAGCAGGTAACCAAA CTGAAAGGAACAAGTAATGACTTTCTTGAACAA[A/C]GTGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G			CCTCAACCATCTGTAAACCCGAGCC[A/G]CAGTGAACCGGAGCTTGCTCTCCCATCCAGCCCTCT CCTATCAGCATCCGTAAGCGTCAGTCAGCAGGTG
EST14083 7	23 A G			CAATGGTGTCATGTGAACATAT[A/G]ACCTATTATCAATAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGACCGAACAGGAGGTTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAAATATTTT	AATATCAATGCATTCTTGTGGCATGCTAGACAGAGGCATTAT[C]JTTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTTCCTTCCCTTACACTCATTTTAAATGT
EST14812 2	50 A G	CAAGTCAGCTT CTACATTCTGA	TAAAGATTAC TTAAATCCCAT	TTCACTTAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAATCTTTAGAAAGTCCCGAGTTGGCTTTTCTAACATTTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGTGATT
EST14815 3	128 A T	CATCACCCACC ATACTGGTT	CGGGAACAACA GTACCGGAA	TTTGCTTCGGCAATACATAGTGGCAATGCAGCGTGAGTTGGCGCGTCTCCCCACTGAACCAAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAACCTTGCCCGTCAATACCCACCATACTGGTT[A/T]TCC GGTACTGTTTCCCGTA

EST15420 6	109 C A ---	GAAGAAGACAA AGACAACAGAG TTATTCTC	GGATAGCTGA AACAGAGATA TTATTCTC	---	TTTAAACCCCAAGACTTGTAGATGTCAGGACTOOGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTGTGTCATCATATAATCATATAGCCAAAGGAGCTC/AJGGAAATTTTGGCTGCTTCAAGTCA TTCCAAAACCTCTCAGG
EST15700 6	48 G C GGA	GGTTTGCCAT CACAAAGC	GATAGTTGATG TTCATTATTCC CTATAA	---	GTCACCAGCAGCTTTTATTAGACGTGAAAGACAAAGACAACAGAGGA[G/C]AGCAGAGAAATAATA TCTCTGTTTCAGCTATTCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATCTAGTAGTA
WI-16739	57 G A	GGTTTGCCAT CACAAAGC	GATAGTTGATG TTCATTATTCC CTATAA	---	AAGGATTGAAACATACCTAGATCATATAAATTTGTGAAGGTTTGGCATCACAAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAATTCCTCCAAAGGT
WI-16782	96 C T	CACTGTAAGG TC	CTTCTATCTTT CTGTTCTCTCA	---	CTTCTCTCTCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGG[C/T]GATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATTGTGGGG
WI-16783	64 A G	TCCTGAGATGT CTTTTACCTGA	CTGCTTGGTTC AATCCTTATTA G	---	AAAAATGTAAACCTTAGAGGTGCCTCTTTTGTGTCACTTTTCTGTGAGATGTCTTTACCTGAG[G/G] CTAATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C ---	---	---	---	CAGGACTTAAGGTCAATTTGCCTGGAAGACTTAACTAAAGGTGAGGCAACATAGGA[T/C]TGTGA CAGCAACACTCGGACCAGGAAGTGTGAAATCGTCACACTAGCGTGGCCAGCCCTTTTTCCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89 G C ---	---	---	---	GGTTTGAAGACGCAGCTTTATCTCACTGCCACTGGGATCTCATTTTGAGAGCTGTTTGTGAGCC TTTTCCAGAAAGCCGCTG[C/G]GGGTTTCTGAAACCTCTATGGGCATTTTAGAAT
EST16089 9	96 C T ---	---	---	---	CGTCTGAAGTTTCTTTATCACAAGTCACATCAATCCCTCGGGCCCTGCTCAAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC/TAAAGAGCCATCCCTGCCCCCTTCTTGCT
EST16100 1	24 C G ---	---	---	---	ATCCAGCTGTGAAGGGACAGGAG[C/G]GTAAACACAGTCCATTATAGGGGTGTGCACATCCCA GGGGCTCCAAATAATGCAACATTTGTTTCACTCGTCCATGCTGTGATAGTTTCATAGTAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G ---	---	---	---	TTCTTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTGTCAG CTGGTTCTCCAGGGA/A/GTTGGCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ---	---	---	---	ATGGTATAACAAATCAGTTCAGGTTTCTGTAACAAATGATCCTTTGGTCTTTCCCGTGGCATG CTCCTAAAACAACTAAACAAACCCCTCTACGTCTAATCAGTCACCTAAGATA[T/C]CGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ---	---	---	---	ATGGTATAACAAAAATCAGTTCAGGTTTCTGTAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCTCTAAAACAACTAAACAAACCCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ---		AGCCAAATCAAACGAACTCTATCAAAACACACAAAGGCCTAGAGGAGAGATTATCTAATGAACGTT AAATAATTCAGGCAATTTTGATCTAAAGCATTTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ---		CATTGGTTGGGTAGGGAAGATAGTAGTGTGCAATAAATGGTTAAACACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTGAAATTTATTTACTGAGGGTGATAGGCAGAAGTAGTA
EST16183 2b	59 A G ---		GCAGGTAACTGTGGTTACAACGTATTGTTCTTTCATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACGTGCTTCTGCGCCTTCTGTTTCATATTTTATGTCACTGTCTAAACGTGGCCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---		AATCTTAGGCTCTTGGCTTTCAAAATC[A/G]ATACAGACAGATAAGAGCTTTAAGTATTTCCGCAATT CCCCAGAGGAAAAGTCAGCATATAAACACATGGTGCACATGCTCACGCACATGGTGTCTC
EST16229 2c	52 T C ---		TGTGAACCTCGAATTCGCTTGTCCAAGTCTGAGTCACAGTTTCATTGGGAGT[C/CCCTGTGCAGOC CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ---		TGTGAACCTCGAATTCGCTTGTCCAAGTCTGAGTCACAGTTTCATT[C/T]GGGAGTCCCTGTGCAGOC CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
WI-16816	124 A G TGGGGTTA	GGAGCCATTGT GTTACAGACAG	CAGACTTTTCTCACACCTCATTGGCTGGAACCTGGGTGCACATGCACATCCTTGAACATATCATTTGGCAA AGGAAATGGGTATCAAAATTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGTTA[A/G]ACTGTCC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ---		GCCACTCTCCTGTGGCTTGCTCTGCTGTCAGCTGCTGTCCAGTGCCACAG[ATG]TGCTAGCCCTCATGG CAGAAGCATTTTAGCCAACTCCTGCTGCTGCTCCACTCTCTTCTTCCGCCGCTGGGCTCAACCAC TCTCTCTCTCAATC
WI-16824b	83 G A ---		GTCACCCACGCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTG AA	GTCACCCACGCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTT[C/G]TCTTATGAAGAAGTC AGAACTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---		TTGCTTTTATTATCCAGAAGGCATGCTACAGATACTGTACAGCATGAACATTTATTATTACAAA AATGGCTTCCAAACCATTAAAAATGAACCTT[C/G]GAATAAGAGCATAAACCGGAACAGTAACATCA
WI-16857	47 G A A	CAATAAGCA GCTAATGGCA	TATAATCCATCCTCCAACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTTCAAGACCTGTGCTTCAAAATGTTTCTGATTAATGGGAGAAATCTGCTCTTTATGTA

WI-16879	79 C T	GATACAGGCC ATATTTCCCA	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAACAACCTCCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCA/C/TATAGGACTCTAGTTCTAGAAAAGCCTTGGGGAGAACAGGCACCCAG
WI-16882	99 A G	GAAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGTGGGAGAGACAATTTCCCCCTTTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAAAATGCCACGTCTCTGAC/A/GGCGATTTACCTGACATGTGTCTATCTCCCT
WI-16888	70 G A	GCTAACTTTGG GCAGGTC	AATGTTCTGAA TTGACCAAAAT TAA	GTAGTAAATGTTTCATCACTACCCGGGGAGAGCAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC/G/AJTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75 C T	ACTTGGCCTGT GTTGTTCA	GTCATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTTGGCTCCCAACATCAGAACATAAGTTCCATGAAAACAGGAACCTTGGCCTGTG TTGTTCA/C/TCCCACTCCCTAGAAAGATATAGACA
WI-16910	74 G A A	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGTTATATTCGCTATGACTTTTCATCTCAGAAAGATAAAGATGGCG CTAGAA/G/AJGTATCTGTTATAGAAACGATACCTTCTATTTGGCCTGAACCGTGAAGGT
WI-16918	93 C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAATAAACTACCACTTCTCTCTGCTACGACAGAGCACTAAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACCAGCA/C/TJGATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127 A C	GGAAAGCAGA CCTGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAGCTGTTAGAGTCTCATGGAATAGGCCTGGAGCAGCAGGATT TGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGG/A/CJCCA CGGGCAATCACATGAGATG
WI-16947a	58 C G	CATGGAATA GGCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAGCTGTTAGAGTCTCATGGAATAGGCCTGGAGC/GJACAGG ATTTGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16966	43 T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATAT	CATTTGTTTTACTTTAAAATGCACACTACATAACAACCTAATA/T/CJTTAACTTGGTCCAACATATT AGTATAACTAATAGATTTTATACTGATAACTTGCATGCCATTAAA
WI-16995	55 T C	GAGCAGTAGA GACTGAGGTA	CATGTTGATTT CCAGCCGT	TTGAGTCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAAATAGTATTT/CJACGGCTGG AAATCAACATGCCCTCTTCTTCTGTGAAGTTGTGAGCATGGAGCTGAGAAGGCTGAGTCAATCT
WI-16992b	60 T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTGCGCCCTCATCTGAGAT/GJGTG TAGGACTGTAAGGGAATGTTTGGGGTTTAGGAA
WI-16992a	46 G A TC	AAGCACCAG AAGTACACTG	CACATTCCCTT ACAGTCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTG/GA/JCCCTCATCTGAGATGTG TAGGACTGTAAGGGAATGTTTGGGGTTTAGGAA

WI-17010	23 T C	T T C A C A G G A	A A T A A T A C G G T	A T G T T T C A C A G G A A A G C C A T G T C J A T G A C A T T C A A A A C A C C G T A T T A T T A G A A G C T C A T T T A A T
EST17127 9b	74 C T	C A C T C G G C A C A G A C A G A T	G G G A G G C A G G G G T G	T G T T T A T G C A G A C A A A A T C A A G G C T A A C T A A A A G C A G A T C C A A T G A C C C A G T G A T C A A C C T A G A G G T C C A C G
WI-17040	94 T C A	A A T T C T C T T A T C A T C T C A A G C C	G G A C T A T G G C T T A T T C A G T G A T G	C A C G C G T T C A T T A A A T T G G T A C A A A G C A T G A A C A C T C A G G A C A G A T T G G C A C A A T A C A T G C A G T T C G A G A A T T C T C T T A T C A T C T C A A G C C A G T C J C A T C A C T G A A T A A G C C A T A G T C C C A G T C T C G T T T T C C A A A T C T T T C T C A T A T T G T
WI-17044	47 G T G	G C C A A G G G A T T A A C G T A T A G	G G G A T C C C C T T G T T A A G A	T T G T T T G T T T G T T T T C T C C T G C C C A A G G G A T T A A C G T A T A G G T G T J T C T T A A A C A A G G G G A T C C C C A C T T A T A G C T G A C A G A G C A G C T G C A A C C A C T G A C T C T C T G C A G A A T G G C A G G A A T C G A A T C A A A A G A A A A G C A A G T G
WI-17021	62 T A A C T C	T G G A C T T G T C A G C C T A T A A C T	T G T A G A G T T A G T G G C A G C T G C	G C A T G T T G G A G C A G A T C C C A T G G T A A G C C A A A A G T G A C T T G T C A G C C T A T A A C T A C T C T J A G C A G C T G C C A C T A A C T C T A C A G G C A C A G T A A C T A C A C T T T A T A C A G G A G C A C A T G C C A A G T G C C T G G G A G G T G C C A A T A A A T C A A
WI-17065	90 T C T T	C C A G A A A G G A A A A G C A T A A A	C C C A A G A G A C A A T G A A A T C C C T	T G T A A A A A A T G T A G A C A T G G G G A A A A A A C A T T C G T A A T C A A C A T G T G C T G T T T C T A C T C C G G T A C C A G A A A G G A A A A G C A T A A A C T T T C J A G G A T T T C A T T G T C T C T T G G G T
WI-17066	32 A C T	T G T A C A G C C A A C A T C A C T G T T	G A G A T G T T G A A A A T G T T C T G G A A	T T C A T A A G G T T G T A C A G C C A A C A C A C T G T T J A C J A T T C C A G A A C A T T T C A A C A T C T C A A A A A G A A A C T C T G C A C C C A T T A G C A G T C A T C C C T G T A G C T C C C T A T A G G C A A T G G C A A C T G C T G A T C
WI-17074	86 T G ---			T G C T G A C T G T C A T G A C T T A G T A A G G C C A T C A C A G G T T G C C A G A A C A T C T A C T A A C T G T T C C A A G C A T A A C C T C C T A C A C A G G C C T T T G J C T A C A T A G G A G T A T A T T G G C C A A G A C T C A C C A C T A G A A G T G A T T
WI-17104b	108 T C ---			C A G A T G A A A C T C A T G C T G G C T C A T C T G C A A G C T T C C T G A T G C T T T G C G A G C T T C C C A T T C A T T C C A A A T C A G A A G C A G T C A G T G G C C C G T G T T T C C A G A C G G C T T T C J C T C T T T G T T A A G A A A T T A
WI-17114a	37 T C G A C T T T G T T T	T T T C C A T C A A G G A C T T T G T T T	T T G T A T T A A A T A G C A G A G T G A A G A G A C	A G C G T C C A C A G A T G T T C C A T C A A G G A C T T G T T T T J C J G T C T C T T C A C T C T G C T A T T A T A T A C A A G C T A C C T C C C A A G G C C A G A T G C T A A G T G T A A A G A A G A G A C T G C A G C C A C A A T C A G A G T T A C A T G G S A
WI-17150	76 T G C T C T	G A T G A A A T T C A G A T A G T C T T C	T T C T C A G A A T C C T G G A A G A T A T G	C G T G C T G G A C T A A G T G C T C T T T C C A T G T G G A C A C A T C T C C A C T G A A C A G A G A T G A A A T T C A G A T A G T C T T C C T C T T T T G I C A T A T C T T C C A G G A T T C T G A G A A G G C C C T C C T T T G T C T G C T C T A A T T T
WI-17163	43 A G T A A C G T T	C A T T T C T T T G T A A A A T A A C A A	C A G A A T C T T G C T T T T G C C T T	G A A A T C G A A T A C G T C C A T T T C T T T G T A A A A T A A C A A T A A C G T T T A G I A A G G C A A A A G C A A G A T T C T G T A A C C A C A C A T T G G A A A G G G G A C A C A G G G G G C A G A G G G A A A G G C C A G A T T T T C A A C G G T T T C C T C C A C A T C T G C A G A C A A

WI-17178	127 T C	GGACTCCCTCA TGAGGAGC	CCCTCAATTTT CAACTGCTTC	AGCAAAATGTCCTCCAAATTTTCAATAGCTATGATGGAGTTATCAGTTCAATTCAGAGCGAAATTACTGG GGCGAGGGGGTTTAATAATCTGATGGGTTAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA GCAGTTGAAATTTGAGGG
WI-17180b	81 C G	--- CACAAAAATA TAGAGAATCC TGCA	--- TGCGACGAGAC TTGGG	TCATGGACATCTCTGAAGCAGACACAAAAATATAGAGAAATCTCGCACTTCCCAAGTCTCGTGCACAG GCTTCAACAAATTAAC/C/G/AACATCTTGCCCAATTTGTTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17180a	47 T C	TGTTCTCTAAA CTTTAGATATC CTCCA	CAAGAAATAT ATATTTGATTC TGTTGAA	TCATGGACATCTCTGAAGCAGACACAAAAATATAGAGAAATCTCGCACTTCCCAAGTCTCGTGCAG CAGGCTTCAACAAATTAACCAACATCTTGCCCAATTTGTTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17156	54 C G	--- CAAGGTTTGA AGGAGGAACA	--- OCACGACGTG CATGA	TGAGGTAGCAGGGCAATCTTAAGAAATGTTCTCTAACTTAGATATCTCCCATG/CJTTCACAGA ATCAAAATATATATTTCTTGTTGGAAATTTAAATGTTCTTAACATATCTGCCTACCATCCACCTCAAT TAATATTTCTG
WI-17149b	79 T C	--- CAAGGTTTGA AGGAGGAACA	--- OCACGACGTG CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAAGTTTGAAGGAGGAACATG/JTTCATGACAGTGCCTG GAAACCCAAATTTGCTATGTGTATGAACACTACAAAGGATGGGGAAGAACACATTTCTCTCACA
WI-17197	67 G A	GCAGAAAGTAG CTGGGGCTAC	GGTGAGGTGGT GCATACC	ATTTTGCTATGTTGCCTGGGCTGGACTCCAGCAATCTCTGCTCAGCAGAAGTAGCTGGGGCTAC/G /A/GGTATGCACCACCTCACCTGCTTATCAGTTTCGTTAATAGAATATTTGACTTTTAGATGCGCA
WI-17198	38 A C	TCCCCCTTGTG CCTAGTTT	TCCATTTGTGC ACTGAGAAATTT	TGTATTTCAAGTACTTTCTCCCTGCTGCTAGTTTAC/JAATTTCTCAGTGGACAAATGACAA ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGACACATCC TTC
EST18753 8	27 C T	CTACCCAGGCT GGTCTCAT	GGATCGCATGA GCTGA	TCGCTATGCTACCCAGGCTGGTCTCATG/JTTCAGGCTCATGCGATCTCTGCTCTGCACTGGCTGG GATAAGACACAACCTGCCACCAGGCTGCCCTAGGAGTAGTCTTAATGCCGTGATGGTGGG
WI-17108b	74 C T	GCAATTCAGTC TCAAAGTAAA CA	AACTACGATTT ATCATATGCTC CC	TTATTTTAAAAATAACAGATGCACCTTGGTTTACATCTCTGTTGCCATTCACTCTCAAAGT AAACAC/C/JTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCATAGCAGCTTACAGAGT
EST19087 2b	41 A G	--- CGTGACCAATTT AAGGTATAG TTC	--- AAAAGTTGAA TGTAATTAATG OCA	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTC/JAGTGGCATTAAAGTACATTCAACT TTTTGAGCAACCCGCCCATCACTTCACTATCCATCTCCGTT
EST19125 8	28 A G	--- AAGGTATAG TTC	--- AAAAGTTGAA TGTAATTAATG OCA	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTC/JAGTGGCATTAAAGTACATTCAACT TTTTGAGCAACCCGCCCATCACTTCACTATCCATCTCCGTT

EST20824 8	115	T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGGAAGCCGGAGTTTATTATTATTAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGAGTGCTGATTG/GTTCGGGTCCAAAGATAAA ATCTTAGG
WI-17347	50	A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCTTA/GGTAGCACAAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGTGAGTGGGACCA
EST21904 b	128	G A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTG AGAAAGCAT	TGATTTGGGTCTGGGAGCAGGTGGGCAGTTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAAACAGAAAAATGTACTAGGCTTTCATATGGCCATTTTAAATAGTG(G/A)TA TGCTTTCTGAACACCTGCC
EST22111 3	82	T C	GAAGATCTGT CTGGCATTCCT	TGGA AAAACA GCCCCAC	CAAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGTCTGGCATCTTTTTC/GTGGGGCTGTTTTCGAAGGCACA
EST22197 2	78	T C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGCGGT	GTTTAAATGATCACTCACCAAAATCCACAGGAGAATCTTAAATGTTTACAAGCACCAATTTATTCTGCT ATTCCTGCCATT/CJACCGCATCCTTCATGTTAGAGTATCACAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92	T C	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAATCCACCACCTGTAAACAG TAGCATTCAATGGTTTTACTCTA/TCTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54	A G	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAATCCACCACCTGTAAA CAGTAGCATTCAATGGTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41	T C	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAATCCACCACCTGTAAA CAGTAGCATTCAATGGTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19	A C	---	---	TCGAGGAGCTCTGAGGAGC(C)CACCAAGGAGCTGTGTCCAGGGCCACCCTGCAGGCAAGTGTG GTCCAACTCCTCCTCCCTTTACAAAACCTCCAGCTCACCCACACAACACTGGCTGACAGGCCCTCT TAAGCCTTTTAACTGT
EST22433 c	103	A G	AAGACATGTT CACCAAGTGA AA	CAGCTTCAGCT TAAC TGACAGA AGTTTCAGTTT	GATGTTAATGACTTCTCTTGGAGATATGATGGAAAAATATTCAGGTACACATGGAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC(G)TGTGCTGAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71	A G	AAATGGATCC TTATCTGCACA	GCATGAATTT T	TATCCATTTCAAGAAAAAAATGACTTAAAAATACAATTTCTATCCAGAAATGGATCCTTATCTG CACA(A/G)CCATTGAAGAAAAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTGTT TCTACCCC	TGCTGTAA TTTGACTGTAA TG	GGCTTTTATTGCTCCTTTTAAACATCAAAATGTTTATAACACACTTGATCCTTTTGTCTACCCCA ATTTCATTACAGICAAATTAACAGGCAATATAATAGGCTAACAGAATGCTTGCAATT
EST23021 0	108 T A	---	---	TTATTCTCAGCTTACCATTGTTGTAATCTCTGTACAGGTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAAATTTTATTAACTCTTGCCTTTTATGGTTTGTACAGTTTGTGCTCTTCT T
WI-17387	55 C G	CCTTGCAGAT TGAAGAAA	GCTTTGCCTA AGATTAATAGT AACTACT	ACAGAAATTTAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTTG
EST23869 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCCTCC TGTAAGC	TTTTTGGCTTGTCTGCAGAAATAGATGAAGAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGCACACTAGGCAATGTAAAGCTCCAGAGGCAG/C/GCTTACAGGAGGGGAAGGACGCTGAGGC CAAGAGTCTGGCTCACTG
EST23733 9	31 T G TT	GGCTGTTAGTT TTGTTTTGTTT	TGCACITTTAAA TCCCATCAAT	AAAGCTGTTAGTTTGTGTTTTTGTCTTTCCTT/GJTATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
WI-17470	83 A G CCAG	GTCCGCTCCCG CCAG	OCAGTGACGAG GOOGA	CTGACACGTCCTGTGTGCGGGGTGCTCCATGTGCGTGTGTGAGTGAGACTTTTACTGCGTCC GTCCCGCCAGCCCTT/GJTCGGCCTGCTCACTGGCCTTGTATTTCTGTCTTGGTTGGAAA TACCATCAGCCTTCC
WI-17519	55 T C A	GTGTCCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAATGCATTTGTGCTAGCTAATGAATGCAT/CJAGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAAGAGCTTAGAACAGTACATGGTGCATAG
EST25356 3b	95 C G	---	---	TCTTTGATACAGGTAACCAAGTTTGTAACTATTTCAGAACTTCACTGTATCTTCAAGTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GJTATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	---	---	TCTTTGATACAGGTAACCAAGTTTGTGTA/CJACATTAATTCAGAACTTCACTGTATCTTCAAGTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAATGATAGTAACCCAA/CJTTAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT CATTTGATAA	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAAT/CJGATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCCITGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAATGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAGGCCTACT TCCTTGTGTAACACTCC/CJGATATTGTCGATTCTAGCTATAAGAAATGGGCGCCACTAAGTGGGTC

WI-17623	46 T C ---	---	---	TGTGGTTTAAATTTAAATTTCCCATATAAATTAATGGTGGGCACATTTC/GCATGTGCTTACTGGGTC ATTACATATATCTTTGTGAAGCATCTGCTCCAATCTTTTGCTGACTTTGGAGTTTTTGGT
EST26419 1b	46 T C ---	---	---	ATTTCATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGAT/CJGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTGTAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35 C A AG	CAAGAAAGTTTG GACTGCC	ATACAAAGGC AACTATGTGC	ATTTCATACAGAGATACAAAGGCAACTATGTGCAG/CJAACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTGTAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780 5	69 G C ---	---	---	TCAGCTTTAATTTAAGGGACATGTAAATAAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC AG/CJAGGTAGACCAGTAAACAACCAAGAAAGCAAGTCTGTTCCATCTTGGCTTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---	---	---	TACTTCAGTTTAAGGCAATTCACACAGAGACTGTCTC/GJGAGACGGGCACAGAACCCAGACACC GTAGAAACACCAACCATGCATGACGGGAAGCAGAG
EST27152 1	101 C T ---	---	---	CAAAGGATTTATTTGTTCCCTAAAGTAAATCTAGAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAACATTTCAATCATCTCTCTCTC/TJTTACACATGGTGACTCTTTTCATGTACACAT CATCGGAAACAGACTGA
EST27504 0a	33 G A ATTT	GCTGGTGTGAT GCTACTGTAAT G	GCACTTTGCAA CAATTTAATA	TTTTTGCACTTTCGACAAATTTAATTTATC/GJA/CATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTCAGTATTTCTGTACACATTCCTGTTAACAGAACCCCATACATT GGTAAATTCATCT
EST27662 4	51 C T CTCCAGTCTTG	TTATGGAATG GCTTATGTAAC C	CACATTCTGTT CTCCAGTCTTG	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTCCTGTTCTCCAGTCTTG/C/TJAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAACACACACTCTTGTAGGAATGTTT
EST27788 3	100 A G ---	---	---	ATTTTATTAGCGGTACAATTCGAAGGTGGTAAGGTGAAGGAAGGGGAAGGCAGGCAATACAT TATTGAGCTGAAAACAACTTTACATTCGAAGGAC/GJGCTTCCAGACAAGCCATGTAGAACCAGCAT GCTTGGGACTGTGTGGAT
EST27828 4	58 G A AGAACCCAC	GTGCAGAGAGG TACTCCAAGTA C	GGAAGTCATC AGAACCCAC	TCCTCTAAAACCTTCTCTGTTGGATCCAGTGACGTGAAGTCAAGAACCCCAAC/GJA/GTACTT GGAGTAOCTCTCTGCACCAAGATAGTGGCTGATTTTCTGCTCAGTCACAAATTTACTTGAA
WI-18369	58 G A ACAATC	TAAGAAGGCC TTATCCATT	AATAAATTC AATCTGTCAC	TAAAAATTTGAGATACATTCCTCCCAATGTAAACAATAAATTTCAATCTGTACACAATC/GJA/AAATG GATAAGGCTCTTGACAAATTTCTGCCACCTCGTTTAAAGCATCAGAACTCAATCTTATCTC TCCGCTTCCAAAGCTTTATTGGCAATATGCTCTA/TJ/AAAAGAATGATCAATCCTGTGCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACACCCAGCCGCTGCTGAAGGAGACTGCTGTTGTG TCCACCTCTTATTCATAG
EST28036 4	37 T C ---	---	---	

EST28483 7	31	T A	GGAGTAAAG GTGTTCTTCT	TTTCTGCGATT TATTTTATAG CA	CATTGGAGTAAAGGTGTTCTTCTTTAAATTAATGTAATAAATAAATGCGAGAAACATTAAAC GGAGAAATGTACAGACACAGACAGACAGATGAGTTGTTCTGACTGTGACACATTGGGTGAAA AGAAATGGTCTAGTAATCGTTACAGGATTTCGGTGATGGGCCCTCCCTGTCTCTGCGACACTGCCAAOC CACAGCTGGAGGGGCACTTAAGCACGTCATTTTGTGATTAGA TGAGCCTGGGAGAAAGACACAGAAAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATACTG TTTCCACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTGTCA
WI-17724	50	T C	TGGGCTCC TGTC	TGGGTTGCGAG TGTC	
WI-17730b	68	T C	---	---	
WI-17730a	39	A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACACAGAAAGTGAAGTCTATTAGTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTGTCA
EST29041 5b	53	G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAACACATTAAGCATCATTTGTCACTTG/AJGCTAACTCCT CAAATCAACAATACCCCTTTATTTTAGCCATGAAAAC
EST29128 4	58	A G	---	---	CTTTAGAGGACACACAGTCTGTTGGACTTAGGGCTACCCCTATCCAGCAGGTGCC/A/GJTATTT TCACTTGGTTACGTCTGTAGGACCGTTTCCAAATGAGGTTACAGTACAGGTTCTGAGCAGACATGA GTTTCTGCTGGGACACT
EST29912 3	103	C T	TCGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATCTCTG T	ATTATTAGTATCTGCTGTTGGGGTGGGGTGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCTCTACAGAAAGATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121	G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAATCTTAAAGTTAACTCACCATGAAA TTTAACTTCTGTAAGTCTGCTGCTGCTGATGAGGCAGTAACTACATAGGGATAAA/GCJAGCTCAGTA TCTGGAATCATGCTTCTG
EST30223 2	99	A G	---	---	AAATAAATACATCATGCGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAGCAA TCCAAATTACACTCTAAGTTATTTAATATTCCTA/GJGGATTTAATTTCTTCTAGTTCAATCTTGGGA GG
WI-16260b	86	G A	---	---	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAGACCCAGA GTTTCACAATATAGTAGTG/AJATAACCAGGCTCTACCTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59	G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAGAA/GTJACCC AGAGTTTACAATATAGGTAGCGATAACCAGGTTCTACCTTCCCTTCCGTGAGAACTTCGTGGGAC AAGAGAAACAGGAATATTGTGCTTCTTG/GA/GJGCTGTTTCTATACCCCAATATCATATAAGAAAT GTTGTGCTTCTATAATGTTACAGTCTCAATCTTTTGCTTAATCAATCCAAATGAATACCTGAAT TTCTCCTCTTGTTCAAA
WI-17835	30	G A	TG	TGGGTATAGG AAACAGGC	

EST31951 4	87 C T	GGGTGTCCAG CCAACA	CCACCAAAAT CACCTCC	ACAGCCATTTATTATGTTTACTTGTGTAATATCAGAGACTGAAACATTTTCACTCTTTAGCAATGACA TCGGGTGTCCAGCCAAACAC/TJGGAGGTGATTTTGGTGGGAATTTCTTATCACAATATTCT
EST31968 8b	95 T G ---	---	---	CGAATTTGCTCTCTTATTTGTGATTCTAGTAATCCTAAAGATTGGGGGCGGGTTACTATAAGT GCATTTTATAATGCGGATTTTCTGCTT/GJAACTGCCCACTGATTCTTACATGGGAAAGGTGCAAG ACAGTGTACTGCTCC
EST31968 8a	75 T C T	GCGGGTTACTA TAAGTGCAATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGCTCTCTTATTTGTGATTCTAGTAATCCTAAAGATTGGGGGCGGGTTACTATAAGT GCATTTTJ/CJATAATGGGATTTTCTGCTTAAGTGGCCCACTGATTCTTACATGGGAAAGGTGCAAG ACAGTGTACTGCTCC
EST32063 2	103 C T ---	---	---	TCATGGATGAACAGACGCTACCATGCCACATCCGACTTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGT/CJTTTCAGGCCCATTTGAAATAGCAACCGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G ---	---	---	AAGGTTTCCAAGCATCAAAGGCACCTGGGTGTGCTCTAAGTTTCTGGTCACTGCAGCCCG/AG JTCTGTATTAGGAGACCCCAAGCCCGAGTAACAATATGGTCTTGCAG
WI-17800	29 C G	GGGAGCACAA GAGAACTCA	TTTCTACAAT TAATCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT/CJAAAGACTGGGATTAATTGTAGGAATATTTACAG TTTCCACAAGTCAGAAAGAGCTAATCCCAACCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCAATTCCTAAAGTCTGGGATGACTTTCCCT/GJATTTACATCAAGTAGAACCTAAGCCAAAT TCAGAAATCAGAAATCCTTTTGTCCATCAAAATCCAGCTAACTCCAAGCTGAATTAATGTTTCAATCT GTATCTGATGTAGTTAOCATGGCCTGTCATGATTATTTGCTATAAGGAAGGGAAACAAATCTTTA TAGTGTCCAAAGATAATTAATTTCTGGTTAAATCTTTGCCAGCAAGCAAAAT/TAJCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17860	121 T A	TTTGCCAGCAA AGCAAATA	COGTTGTCAC AATCACACAA A	CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAATTTGT/ATTTTGTGTGATTAGTGACAACG GGGAATCTACAATGCTCACATCACAGTAACCTACCA
EST33301 4c	43 A T	ATTGTT	---	GAAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCATGATTGCTCACACAAGCATGATC AATCGCCACGAGA/GJAACTGGATGCCAAAGAGTATGG
EST33301 4b	80 G A ---	---	---	GAAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCATGATTGCTCACACAAGCAT/GJAA ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	63 G A ---	---	---	CTATCCAAAGATATTTATTCAGCGGTGGTTTCAATACTAAACA/GJATGTAACAATGCAAAATTT TAACAATAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAATACTTTGCAA
	44 G A C A	AGCGTGGTTTT CAATACTAAA	CTGTATTTATT GTTAAATATTT GCATTGTT	

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACACIAGJTACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACAAACACACAAATGA
EST34149 5	69 A G A T	TGCCAAATAC TCAAGTGTGA AT	AACTACTAGCG AGAACAACTA ATAAAATC	GTITTTTCTTTGAGTGACACAAGCTTGTTCATTTTGGAGAAAATGTGTGCCAAATCTCAAGTGTGAA TJAGIGATTTTATTAGTTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A	---	---	TGGGAAAACATAAGTTAACTCAAGAAATATATCCAGTCTTTATGTTACTAAACATTGTATATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTCJATACAAAGATTAAAGAAACATTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C T	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTATG TGATAATAACT CCTTC	GGTACACAATTTTAAATGGAGGAACCAACAGGTATGTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCCTAAAGC/CJTGGAAGGAGTTATTATCACATAAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118 A C	---	---	CTCAGTAACTCCGGTGTATAATCTGCCATTTATTGATTTATTTATGATAAAACAACTCTCATTTGTGA AAACAGCTAAGGGTGACATCTOCAGACCCCAACCACTGCTCCTGTATATGTCJCTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84 A G	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAACAAACATCTCCCAGGCCCTCGCAGT AGAGGGAAGGGAACAG/CJGCTGCCATGTGCTCTCTAAAGACGCCACCTCAGGTTGATGT CACCTGTGGGAGACCGGT
WI-17136	33 C G	---	---	ATTCTTTATAAAACACCATGTCCCTAAATGT/CJGJATCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCT
WI-18041	24 A C	---	---	GCCACTGAAAAAAGGTGCTCTTCQ/CJGJBTCTTAACCTCCCTGGACTCCCTCATTTGGAACTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACTTAATCA
EST35164 8a	57 A G	CACAGCCCTGC OCCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTCAAGCACAGCCCTGCCCC/CJGJCTTTGA GATTCAGAATCCAGAGGGTGTCTCAGTCTTGTGTTAGGTGCTTCTGTGACATTTCTCTTG
WI-18052b	67 A G	---	---	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTTCTTTTCATGTACGAATC/CJTGTTTACACATCTT A/CJACAGCAGAGCTGCTGAGGGAGGGTGTGTTTAAATGTGATGCATGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTT
WI-18052a	50 T C A T C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTTCTTTTCATGTACGAATC/CJTGTTTACACATCTT AGAACAGCAGAGCTGCTGAGGGAGGGTGTGTTTAAATGTGATGCATGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTT
WI-18054	46 G A G A G A T A A A A	GGGAGTGGGG GAGTAAAA	CGTCACCCCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAA/CJGTGGAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTTTGCTCAGGTTGTTAGCAACAGAGGTAATG

WI-18064	54 G A	GTAGTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCCTGTGGGTAGCTGCTAAGCTGTATTTCAGAG/GA/GAATGTTCAC AATCATACCACTGGGGAGAAAGAGTAAGCACAGTGTATTAGGTGCCAACTGGGGTACCTGGGAG GCAGAA
EST35347 2	97 T C A A	GCATAAAATT TTCCAGTTGGT	CCCTCGGCAOC TGCT	TTTAGCACCAATTCTTAGTGGAGCAGGATTCTTGATCATGGGGTGAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTTCCAGTTGGTAAGT/CJAGCAGGTGCCGAGGCTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C	AACCCACTAG TTACTCAGAGT GTGTAT	AAAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT/CJATATTAACACATGAAAGATATAATCTTAGAAAA ACCTCCAGTTCTTATTAGTTTGATATTTCTGTACTCAGAACGATTTTAGGTTGCAAGGATATAA
WI-18080c	80 C T	---	---	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCCGTG TTTGACITTTAT/CJTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTGGTGTAT
WI-18080b	65 G A	---	---	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCC[G/ ATGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTGGTGTAT
WI-18080a	41 T C A G T C T C	GCAATATCA ATATCAAACT AGTCTCTC	CAATTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCT/CJTGTAAATTAATCTACTATGC CGTGTGGACTTTTATCTCTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTGGTGTAT GTGGGCATCCTATAAAAGCAGCCATGTGTGTTGAAACAAATGATATGCACAGAAAGCATCTTCT[G/A] TGGCTTGTACACGGTTTCTTCAAGAGGAAGATGACTAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTGAA
WI-18086	63 G A	---	---	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGTACCTTTGGTATTCCC TTC/CJTGTGGTATGAAAGACAGACCTCTGCTGGAGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115b	71 C T	---	---	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGTACCTTTGGTATTCCC TTC/CJTGTGGTATGAAAGACAGACCTCTGCTGGAGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70 C T T	TTAGTGTACCT TTGGTATTCCC TT	AGAGGTCTGC TTTCATACCAA A	TTTTGAGAAGCACTCTGTAAAGGCAAGATGCATTCAAAAAATGGCTTTGAGGATTAATCTTCTTTA GGTAATTTG[C/J]TAAGAACAATAAAAGCATTTTAAAGTCCACTGCCGCTTAGAAACT GGCAAAATATTTTACATCACACCTGGAATCTGCCCAAGTCTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTATCCAAAGCAGCCATCTTCCGGAAGCTC/JAGJTGAGCACAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18169	115 A G A G C T C	CCATCTTCCG	GAGTTCTGCTT GTGCTCCA	TGAAAGAAGTCGACACAGCGGACACT[G/J]TCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGACAAATCAAGAATGAGCTGGAGACATTAATCCTGGCGA
WI-18190b	26 G A	---	---	---

WI-18190	62 G A	---	---	TGAAAGAAGTCGACACAGCGGACACTGTCTAATAAGTGGAAACAAAGGATGAAGCTAATCATGTGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGAAATGAGCTGGAGACATTAATCTGGCGA
WI-18181	100 A C	AAATATATAC AACACTCCCTT CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	GACAGTGAACACATTGAAACACAAATACAAACACATTAGGAACAAGAAATGTGTAAATCCAA TGTGTGAAAAAATATATACAACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAAACGTA TGTGTTCTTGAAC
WI-18215	78 G A	AGCAGAGTTC CTGCCCTC	CCTCCTCTCT CCCC	ATTCATACAAGCATTTCTGAGTACAACTAGGGACAGGTATTTACAAAAACAATAGAGCAGA GTTCTGCCCTC[A/G]GTGTGGGGGAGAGAGGGGATTTCAGCATTTGGTGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60 T A	AAATAAAGGT TTTCAGGGGT C	AAATAAAGGT TTTCAGGGGT C	CATTTCCGAAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/GAA CCCCGAAAACCTTTATTTGAAATTGAAGTTTTGCTCAGAAAACCTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76 T C	GGAAAACCTG AGTTTGAGATC ACA	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAAAATGCTTAGATTTTCTCAGTATTTTATCAATAGTGTGTAGCTGGAACCTTGAGTTTGAG ATCACATAT[C/T]CTGCTCAGTCTATTCACCTTCTGTGGCATTTCGGCAGAAAGTGGC
WI-18242	30 G A	CCCCAAATGTT AATCGTAACA CTTTC	GCTAACACTTC TACTGTAAACAG CTTTC	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACTTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119 C T	---	---	GCATCAGACATCACCACCTCCTGAAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	---	---	GCATCAGACATCACCACCTCCTGAAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T	AAATAGGAAA TATGGACTATC TTCAAA	TTCATGCATCA TTTGTGCA	GCATCAGACATCACCACCTCCTGAAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G	GCTGTCAGCTA TTGTTATTCA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTGGATATGTGGTTTAGTGTCTATCATTAATTTTGGAAAGCTGTCAGCTATTGTTATTTT AAAT[A/G]TATCTTCTGCTCCCTTTTCTCCTTTTCTGGGATCTCATCTCTGTCATGTTTATA
WI-18330b	66 A G	---	---	AAACATCTACAGCTGTCTTAGGCCATCTGTGAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGG[A/G]TATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTTGTGTGAT TCACA

WI-18330a	49	GA	TCCTGTAAGA AATCAGGGAT AGA	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGTCTTAGGCCATCCTGTAGAAATCAGGGATAAGA[A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAGAACATAATTTTTTTGTTGAT TCACA
EST37584 5	85	TC	AAATTC AAGC CATCTACAAA AGA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAAAATTC AAGCCATCTACAAAAGATTTCJCTCATTTGAGGCCTCCATAGGCTGCAACACATCAAAAGGCATTAC TGTA CTGGAGAGGACTGAG
WI-18327	104	GA	AAACAGCTTT CGTTAGGCTAG TT	CGCATACAATG GCTCAGC	CAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC CCAAACAATGGTGAAACAGCTTTTCGTTAGGCTAGTTG[A]GCTGAGCCATTGATGCGGAGGCAGA GT
EST37624 6b	102	GA	---	---	GTGGCAAGAGCAGCTAAACACACTCAATTTGTCATGAAGTCCAAATACGAACAGTGCA[C]TJGCTGA CCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACG[A]JTTCAATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCATTC
EST37624 6a	58	CT	---	---	GTGGCAAGAGCAGCTAAACACACTCAATTTGTCATGAAGTCCAAATACGAACAGTGCA[C]TJGCTGA TGGCCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACGTTCAATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCATTC
WI-18357	89	CG	GCATCAA	AAGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTACCGTGTGAGGTGGCCATGAAGCCCAAGCCCATGGAGAGACATTTTCAAGA TAATCCAGCCCTTAGCATCA[C]GJTCATCTTCACTTTGAGTCTTCCAGCCAGGTCCAAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117	AG	---	---	TTTTATCTGGGTGAGCTCTCTTAATGGCCTGAAGTCACTCTCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGA[A]GJGTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	GA	---	---	TTTTATCTGGGTGAGCTCTCTTAATGGCCTGAAGTCACTCTCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGA[A]GJGTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	CT	GCCACTTTTGC CCCTT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGGTGAGCTCTCTTAATGGCCTGAAGTCACTCTCTTTCAACTTTCCAGACTTGGAA AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
WI-18012b	46	TC	---	---	TTTTATCTGGGTGAGCTCTCTTAATGGCCTGAAGTCACTCTCTTTCAACTTTCCAGACTTGGAA AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75	AG	GCAAAAAGGA CTCTGCATTG	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATTCCTCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTGT[A]GJATTAAGTTTATTAAATCAGCTGACTTTAGCATTTGGAGATTATCTGGAT

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCCTAA	CCCTCAATAAA TCTCATGTCT CA	CCAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAAAT/CITGAGGACATGAGATTT ATTGAAGGAAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAA TTTGAAAAACATTCC TTATTCAATGTCTATCTCACACATCTTTATTATTATTGTTTTCACCTTTCTCAAAATATCGGATTGTTC TCATGAGAATAATGGCTGAGGAGCTGGCACGCGCAGTCTTCTCA/GC/GCTCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	---	---	TTATTCAATGTCTATCTCACACATCTTTATTATTAT/CITGTTTTCACCTTTCTCAAAATATCGGATTGT TGCTCATGAGAAATAATGGCTGAGGAGCTGGCACGGCAGTCTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATCTTTAT TTTT	CGATATTGAG AAAGTGAAAA CAA	GCACATACTCACTCAACATCTTCAATTTGTTGATTGCACAGCATGGCTAAACG/GJTTAAAGATGGGAATCAA CAATACCATTTGAAGATATGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT AACTGAATGGCAGTGAAAAACACTACACATCAAAACTTAGGGAATGTGTTAGTGTGTTACGTTGAG GGAAAACTTATAACCTCAC/GJCGCTTGTTCACAAAAACACAGCAGACAGAGATTTCCAATC CAGCAATGACAGGCTAGGG
EST38909 5	47 A G	GTGAGGGAA ACTTATAACCT CAC	GGTATTGTTG ATTCCCATCTT T	TAACATTCOCATTGAATCCCTTGGTGGG/GC/JGGGGGGGGTGAGATTGCAGTGCTCAAGATAAA TATCACAATATATCAAAAACCTTCAAATTGTCTATGCATTCACACACTGACATGAGCCACAAAACAT CCTTTCACAGGGACTGAC
EST38911 9	85 A G	GGTGGGG GAC	GAACAAGCG	CCTGCTATGATGCCTGGGCAGATCCGGACCTTCGGTGACQ/GACAGGCTCCCTGCCAGGGCTTGG CCCTGACCGGGCTCCCGAGCTCGCCCTGACTGTGTGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST38955 5	30 G C	TGAATTCCTT GGTGG	CACCTGCAATCT CACCCC	CACGTGGCCCTAAGTTTCGGGTCTCCTCAGTCTGGATGGCTGTGTGGAAGAAAGCTTGGTGGTAAG GCCTAAGGAAT/GJAGGGGCAGGGGGCGATGCCGCCAGCGAGATGGTCTGTAAAGCCTGTGGGTG AAAGACCTAAGTCTGGA
EST39002 0	42 G A	GGACCTTCGG TGACC	CTGGCAGGGAG CTG	AAAGATAATGTCTATCACAACGCAACATATAGAAACATAAAAGAAAAATAAAGTATCCACCCCTAAAT CCCTATTATCCATGATATTTTCAT/CJAGCAACTAGTATATATCAATATATTTTTCACAAACCCT TCAGTTACAC
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG GGC	GGTTGCTTTTCATCTTCTCATCTTCTCAGGTTCTGGTCTTGTCTCCTCAATTTTAAACACT T/CJCTTTTATATAGGGAATAGCCCTTAACTGTGGTACATGCTGCCAAAAATTTCTCCAGTT
WI-16398	90 T C	TCA	TTGATAT	GGTTGCTTTTCATGATTTTCTCATCTTCTCAGGTTCTGGTCTTGTCTCCTCAATTTTAAACACT T/CJCTTTTATATAGGGAATAGCCCTTAACTGTGGTACATGCTGCCAAAAATTTCTCCAGTT
WI-16403	69 T C	ACT	AAAG	GCCTTTAATGGCTACAGAAAGG/CJGGTTTATTCTTTTAAACACATCTGGTCTGGCAGC AAGTTATATTATGCATTTAGAGCAATAGGTGCCCTGAA
WI-16406	24 T C	AGG	AA	GCCTTTAATGGCTACAGAAAGG/CJGGTTTATTCTTTTAAACACATCTGGTCTGGCAGC AAGTTATATTATGCATTTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGATTGTTTCATCTGAGAAATAAACTTCCTGTCTAATTTTCCAA/C/GJACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGCC	GCACAAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAAATTGTCTGAGCCAGCAACCTCGAGTTACCCGGCCTTTACCCACGCC AGCTCTGCTTGCTGCAT
EST39366 2	72 T C	---	---	AGAAACCATTCCTGCTGATCAGAGGAAAGATGTATGTAGAAATCAGAATCTGACTGAATTCCTAAA ATCTATT/CJACACTGAGAGGAAATGGAAGAAATGTTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGGTTGAGA
EST39371 9	86 A G	CATTGGATTA GGTGAGG	TGATTGAGAC ATTTCACATTT TT	AAAAAGCTGTAGCTGGCAAGTCAAGTTTATTTATGTGTGTAATTTCCAGTTGAGCATTTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAATGTCTCAAAATCAAATGCTTCTCTTCTAAAGATTA GACATTGCCCAACCTGC
WI-17177	23 A G	---	---	ACAAGTGACATATCCAACCAAC[C/A/G]TCCATCCCACCTGTGCCCTATTCTTCTGTGTTCTTT AGAGCCTTTTCAGCTATTCTCTGTGAAGCAAACTGCACGAAGCCCTCCCGTACTCTCCCTCGGAA G
EST39428 8	31 C T	GCTCCCCACA ATTGATT	GGTCCCTTATG AAGCCACC	AGGTTCTGTTGCTCCCCACAATTTTGATT[C/T]GTGGCTTCATAAGGGACCCAGGATTCTGCATT TTCTGGTGGGCTAGTAATTCTGTGCTTGTGTCACAGAGCAACAATTAAAGAAGATCAGGTCT GGCTGTGC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT C	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/A/C]CAATACCCCGACCCCTGA CCCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGGACTTCA GAGTAA	TCCTGGAAAAC TGACATAAAC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTTGGAGAAAATAACAGGAACCTATTTATAT ACGTAATCACTTTCATACCTGCTACTGACATAGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTCCAGGATTGTTCTCC
EST39465 2	80 A G	AATGCAGGAG GGTGCC	CAATCTGGCC CCTCT	ATGGTGCATTAGAGGGCCACAGGGGATGGGGAGTAAAAAATAACATAAACGAACCTGAACAGAAA TGCAGGAGGTGGC[A/G]AGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G	AAAGATTCT GTAGACATCT AACATTAG	CAC TTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTGACACATTTTGACCAGCCATAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATTGCAAGTTCAGATTCAAGTCAACCAATTC
WI-18387b	84 A C	---	---	CACAAAAATGGGACTGCTGAAGAGTGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGTGTC CATGCTTTAGCCATAC[A/C]CATGTGAACATTGACTATGGAGTCTTGTGAAAGTGTAAATGTGCGGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCTTACTTTGG	GCTAAAGCATG	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACAGTITTTGTG
EST40601	78 A G	GGTGGAAACCT	TTCTTGGGAAGA	GTACATGCTTTAGCCATACACATGGTAACATTGACTATGAGAGTCTTGTGAAAGTGTAAATGTGCGATG
9		GAACAC	AAGCGTC	GCTATGTAGACATAAAGA
EST41935	32 A G	AGTGATCAC	GCACACCTTC	TCCAGGATGGTTTATTCAAAGCTGTGGACGGTGAACATTAAAGACGAAGAGGTGACTCGCGTGGGA
		ATCTTCAGGAT	ACACTGTTA	ACCTGAACACAG/GGACGCCCTTTCTTCCAAGAAGGGCTGTGGCGATCAGGCCCACTCAAGG
		AGGT		TCATTCAAGTGTATCACATCTTCAGGATAGGTAG/GATACAGTGTGAAGGGTGTGCTCATTTTCTTC
EST43091	28 C T	CATTCTGGTCT	AAACTGATTT	AGCTGTGAGTAGAGGAGTCTTCCGAGAGTAGCAGTTGTGA
WI-18420c	108 T C	TTATTTTGGGA	GTAAACATG	ATGTCATTCTGGTCTTTATTTTGGACA/C/TGTAGCATGTTTAAACAAATCAGTTTTTTCATAGGCAA
		CA	CTAC	CCTTTGAACATCAAAAGAAATACAATATATTTTTCACAAATTTCTCATCACTGTAAATTCA
		AGGAAGTTTC	AAATCTCAGC	AGAGAGACAACAAGAAGAAATAGGGAAATGGGAAGAACAGAGTGAATTAAGCAAAATCTTGGGA
		C	ATTGCTATAAG	TTCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAA/T/C/GCTTATAGCAATGCTGAGAA
		C	C	TTTCATAGGTACTTCATGGGA
		GAATAAGGGA	CCAAGATTTGC	AGAGAGACAACAAGAAGAAATAGGGAAATGGGAAGAA/C/TJAGAGTGAATTAAGCAAAATCTT
WI-18420a	38 C T	AAATGGGAAG	TTTAATTTAC	GGATTCAAGATTCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA
		AA	TC	TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C		---	AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCCTGTC
		CACCTGTCT	CCTCCTGTTGT	CTAGACAGATTCA/C/TJGCACACAACAACAGAGGAGGTGGGGTCAACGGCGGAGAGCCAAAGAC
		AGACAGATT	TGTGTGCA	TAGGGC
WI-18425	81 A C	A		AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCCTGTC
				CTAGACAGATTCA/C/TJGCACACAACAACAGAGGAGGTGGGGTCAACGGCGGAGAGCCAAAGAC
				TAGGGC
				AAATTAGGTCGGGTGGAACATATAAAAGGAAGAAAGAGAAGTAATCAAGGGAGGCCAAAGTG
WI-18449	129 C T	AAGTGGGACT	GTATCCAGA	GGAAGCTGTATTGCTGATCTAACGTGCTGTTCCAGTTCCTTTTGGCTCTAAGTGGGACTA/C/TJTC
				TGGATACAGTCAGGGGAG
				ATCGCTTCAATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTGGCCCCCAAGACATTATTTTATCTT
				AAATGTCCAATATCTGCCTGATGTCTGTTTGTGCACATTGGGGCCACAGT/C/JAAATAGGCTAAA
WI-18457	120 T C	---	---	AGGCAGTCCCACTGCT
				GGTGTATAGCTGCTGTACACCACAATGGCAGAGGTGA/JGTAGAAACCATCTCAAAGCCATAAAA
WI-18462	39 A G	AGAGGTGA	AGATGGTTTCT	TATTTACCATACATCCCTCACAGCAAAAGTTTGCTAATCTCGGGTTTAGGGACTCCATTGAG
				TGAGGACGTGTGACAAGCTCCAGCAGGGGTGGGGCCGGGCTGAGGGTGGGGTGGGAGG/C/TJGGT
WI-18476	60 C T	GAGG	GTGAAC	CACTCCCATGTCGCCCTGGCCGTCCCTCCACTCACCCACACCTGGCCAGTCCAGCTTGAGGT

WI-18491	109	G A	AACAAATGGT AGGTGGTATT	CGTGTGCATT TCCTGTAATCC	CTAATGAGATGAATACATGGAAGGCGTTTAGCACAGTGCCTAAACACAGTAAGTAACCAACAAT GGTAGGTGGTATTAACTATTATTAAATCCAGAATGAC[G/A]GGATTACAAGAAAATGCACA CGT
EST50757 b	79	C T	GAGCTCGAGG CTGCTTCT	ACCCTTCACCC GCCC	AGCCCCCTCCACTCCACTCTGCTTCCACAAGTCGGCTCCCGAGAGCTCGAGGCTGCTTCTTTTATAT GTGCAGGGCC[C/T]GGGGGGTGAAGGGTCAGAGA
WI-17675	103	T C	GGACATTGG ATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCAGTAGAAACTAAGATCTTCCACAGGTGCTGAAGAAAAGTGTCTTCGTTTTAAT TGCCAAAGCAGGATGTGACATTTGGATGGTGACTT[C/C]CTGGGTGGTTCCCATAGATTACCCAT TGCTCTAATGTGTCTA
WI-16543	87	G T	AGATAAACTA CATTTGGGTT TCG	GATTCATCATT ACAGGGGACTT	GATCCATTACCTAGGGTAAATTTCTCTGAATGTCAAAAGAGATAAACTACATTTGGGTTTTGG G/TAAAGTCCCTGTATGATGAATCAAGAAATCCTCAAGTCTGTCTTGCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAGG TTGGGGAA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCAAAACCATCTCCCTGACCCCGAGTCCATGGAAAAATTGTC TTCCACAAAACCGTCCCTGGTGCCAAAAGGTTGGGAA[C/G]TGTGCTGGTACAAAAAGTAATT G
WI-17690b	79	A G	AGGCATTTTC TAGCTGTGTT	...	ACAACATGTGAAAGAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTGATT GGCTTCCCTAT[G/G]ATTACAGGACCCATAACTCTTGTCTCACTCATCTGCTATGCTGCTG
EST51717 b	63	G A	GCGGAAGACA GTGAGCTGTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTT[G/A] TTTGGCTTCCCTATAGATTACAGACCCATAACTCTTGTCTCACTCATCTGCTATGCTGCTG GATCCAACTCTAGTGTCTAACTCATCCAGATTATTTGAAGTGAACACCCCTCCGACCCCAA TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTT[C/T]GAG CTGGATTATTGCCTCAAA
EST51717 a	39	C T	GATCCAACTCTAGTGTCTAACTCATCCAGATTATTTGAAGTGAACACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCTCAAA
EST53012	97	C T	TGGTCACTTG GGGC	GGCTCTGCCCA CGCC	TTTCCAGTTGACAGGTTTATTCCACCCCTTTCATCCCTCCATGCCCCAGGCCAGGAGGAGACAG GTGTGCTGGAGTCTGTGCTACTTTGGGGCC[C/T]GGCGTGGCAGAGCCACTGGGTTTACATTCTCTGT GGGCAGGTGTGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTACATT TT	AAACTGCAATAACAAAACAGAAGTCCAAAGAAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCCACAAATGTAC[G/A]G/AAAATGTGACAAGATATCCAGATGTTAA
EST53389	74	A/G C A	GGAGACTGC AGAACTTAA GCA	GGCCTTTCTAA CAATAAATGCT C	TTTCGAAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAACAC[G/G]GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAAATAGGTTTTAACATGAAC ACATTAAGGGAGATGGCC

[illegible]

TGR- A003P30	117	C G ---			ACAAAGTTCAAAGGAGAACTCCTTTGTTTAAATGCAGCTGTGCTCAGAAAGCCTGTGATTTCTAGGA AACCATCTGGGTTAGCCATTAGAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATAC
TGR- A004S34	156	C T A			GCTTGTCTTTTATGTTAGTTTCGGGGGAAAGGAAGGGGCTGACAAACCGCAGACATCTGGACACCAGC AAGGGTCCAGGGAGGTTTGACAGACTCTTTGCTCTGGCTAACAGTCTGTCTCATGTGACAATAGCCA AACCTCCTCATTCCTATAAA[C/T]CTTAACAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TGR- A004T44b	97	A C ---			AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAGTCAGGAAGATAAACCCAAAATGAT TGAGTATGATAAAGAAATTTGCATGGCGATT[C/A]AAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TGR- A004T44a	69	G A TGA			AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAGTCAGGAAGATAAACCCAAAATGAT TGA[G/A]TATGATAAAGAAATTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TGR- A004V08	60	T C GGCATTCTT			CCTACAAATCCTATAATATTGCAAGGGTTGGAGGATGCAGGAACAGGCAATTCCTTAT[C/G]GCC TTTTGTGGGAAGGATCAATTTGGTGTCATGCACCTTAGGGGACAATTTGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAAATTTCAAA
TGR- A004V26	125	A G ---			TCTAGCTATAAGACCAGATTTAAATTTCTAGATATAGAATATCCAGAATAATTCCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[A/G]AAGGT TTCAGTTTATAAATGCTTAAATCTGTATCTATTGCTTAAATCTGTATCTATTG
TGR- A004V28 a	29	A G CGATCTC			CCAGGCTATAATGTTGTGGTGCATCTC[A/G]GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCCACCTAACTAATTTTGG TATTTTGTAGTAGAGACATTGTATTTTGTAGTAGACAGG
TGR- A004X20	25	T C GA			TAAGTTTTCCTTCTCTGTAGGA[T/C]GTCCTCATGTTACAGTCAACTATAAACATGGGCTCATGT TCACTCTGGGCTCGCTTCAGAGGAGTTTGATATTTTGGAAAGTGTACCTTTGTTCTGTGTGCTTTTCA GACCAACCGCTTCTTTCATTTCTTCAAGGCTTCCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCCCT
TGR- A004X30	26	T C CCAC			TTTTGAAATCTTAGAGTAGAACCCAC[T/C]ACTCTAGTAATACCTGTAAATAAAATAGATTTT AAACACTTCCATAAAGAAATAGGGGTGCCAGCTCCTTGATTTCCCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TGR- A004Z04	102	T G ATGCAAACT			CACGGTATATGCCCTTATATATAGGTATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAAC[T/G]TTGCTTTCATGAAATTTCTAATTAAAGG ACTGTTGCTTCTTCATATTCATGGACATTATACAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTTAAGACTG

TGR- A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGGTGCAT CGGGAAGA	TAAGTGAGACAAGTTTATTGGAGGAGCTTGACACCCCTCTCTGCOCTAGCTTGAGAGAACAACTGCG AGCATTTTTTCTTTTCTTCTCCGATGACCATCTTTTGGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAGGAAACAGATC
TGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCOG GTCC	GTCTTAGCAGAGGAGATAACTTTGAGGGACAGCCOCCOAGGGGCCAGGTAGCCTTCAGGGGGGGCA GGGTTGGGGGAGGTAGGAGACTCTTGGACCGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TGR- A005D17 c	81 T C	---	---	TATGGACTGTGTAGAAATATGATTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAOCCAGCAAGGCTTCTGTCTAGATTCTTCTGGCCTCTCTGTGAGGATTCCTTCTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGTATCTTACGACAGTCAAACTCTACGACAGTCAAAACAC
TGR- A005D17 b	79 G C	GGGGAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAOCCAGCAAGGCTTCTGTCTAGATTCTTCTGGCCTCTCTGTGAGGATTCCTTCTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGTATCTTACGACAGTCAAACTCTACGACAGTCAAAACAC
TGR- A005D44	97 G T	TTAACATTATT GAACCTTAAAA CTGTACAC	TTGTCTATTAT TTAAGCCCAAC AAAA	CATCAGTAACATATACACAAATGGTGCATCACTGAACCTTGGCTCCAATATATTCTATACAATACTT AACATTATTGAACCTTAAACCTGTTACACTG/TJTJTTTGGCTTTAAATAATAGACAATGATTTTGG TCTATTACTTATGATAGACAAAGTGAATGATTACTTTGTTAGACAAGTGAATGATTCTTTGTTAC
TGR- A005E31b	27 G A	---	---	GGAGTTCAAATTTATAACAGGCCCTCTG/AJCTCACAGCTGTACTGGCTAGGCAAGCTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTTGCTGCTGGCCCTACAAAGCCACCTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TGR- A005E39	182 G C	---	---	CTCAGTGTAACAACTTTGTTTAGGGAAAAAATAAATCCAAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTCTGAGACAGAAATGACCCCTGGGCTCCTTTATTGTTCTTTCAACAGGAOC CCACAGATATTGCGGTATGTCATGAGGACTGGGGATGCTTCTATTG/GC/GGATGCTTCTATT
TGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGTTACTGCACCTTACAGAG/AJCTCAAATTTCCCTGATTTAGGA AGGCGATGCTAATGGGTATGATAGGTGAAGTATAAAATGTTGTTTAAAGAAATCCCAAG CTTGGTATAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAAATAG
TGR- A005E46	76 A G	CACCTGACTCG GTGCTTAC	CCCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGTAAAGCACTACTGCGTATCAGGCACCTGACTCGG TGCTTTAC/AJGTACATTTACCTCACAGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAACTGTCTTAGGGTGTCTCCCAACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGCACTTTGTCTGTCTTACGAGACCTCCCAAGAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTCTTGTATTTGTAAATTTCCCAAGAGCCGCATATGAATCTGCCC

X57830	106	GC	CT	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAAGAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAAGCATATCTGTCATATGCTCTATGCTCTATTTTATCTGTCAAT GAAAGCGGGGTTCAATGCTACAAAATGTGTGCTTGGAAAATGTTCTTGACAGCATTTTCAGCTGTGAG CTTTC
X74070b	72	TG	TGGATC	CTTTTAAAGAA ATTTTGTTTA	GGGCTTAAAAA TATTAGAGATC TAGATT	AACCTGAAGAAGTTACTGGAGCTGCTATTTATATTATGACTGCTTTTAAAGAAAATTTTGTATTATG GATCTG/GATAAAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCTTGGACACTGCAGCTCTTTT CAGTTTTTGTCTTATACACAATTCATCTTTTGACGCTAATTAAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44	CT	---	---	---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGCTCTCATCACCAGTC/TTAGAGCTTCTTCCCGAAGGG CCTTTAGGATAGGAGAAAGGGTTTCATGCACACACAGTGTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGCTAAAGTAAGTGAAGG TCCA
D28513b	133	AG	---	---	---	ATGACCAAGGCCACCACATTTAGAACTTTGGCTGCCCTTGGAAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAACACTTTGGACATGGCTCACAAGCAGTTTGTGATTGACTGCATGAATGCAT GTTGCGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	AG	---	---	---	CCACTCCATCCTGATGCCCAAGTTATCCACAGCCTCTCCCGAACCAAGACCCTATCCACCTGGAAC TCCATTTTCCCTGTAAATCTCCAAGTATCTACCTCCCTACTCTGCAACCCCAAATATGAA CAACTGCAGCAGGTGCCACCAACCAACCAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	AG	---	---	---	CCACTCCATCCTGATGCCCAAGTTATCCACAGCCTCTCCCGAACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAAGTATCTACCTCCCTACTCTGCAACCCCAAATATGAA CAACTGCAGCAGGTGCCACCAACCAACCAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	GA	---	---	---	CTCCCTGCCCTCCTCTCCCTGCTGTGATGCTCCGTCCTCAACAGCCGAAACCTGCTGTGCAATGGGGG GAGGGGGGCTTCTG/AGCTTCTCTCTTCTTGGCTTCTCTTATCTTCCACAAACCACTTCTCAATAAA GCCAAAATCTTCTCTTCTCCCTCAGGCCACCTCCTGCTCTCACTGCTGCTGCTGCTGCTGCTGCTTTT CTGGA
D37931	64	TC	---	---	---	ATTATCGCGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTGTCTC CCCAGGCTGTCTCCTCAGCTCATTTCTACTGTTTCTCTATATAACTCATTTCTTAAATACATT GCACCAAGAGATATGGAGACATAAACCTGTGAATGAATGAGGCTGGCTTTTCTGTAAATAGCTTCC TTT

D63807	101 C T ---	---	---	CAGGCAGGACTTCAGTGCAGTATCCCTGCCCTTCAGTCTCTTTAGAAATCACATCTGTGTCAATCC ATTGTTAGAGGGAGTGATTTTCTCTGTTCAC/C/TGAAGAGGACTTTTGTTCACAAATGGATCAC AATGCAGAGGAGTCTGTCTCTCCCTGCCCTCTCTCGCTGGAGGGTGACCTGTCTCCAGATGAC TGGGAACATGCGTGTGACCTC/T/CJACAGCTACCTCTCTATGAGCTGTTATTGCCAAACAGCCACA CTGTGGGACTCTCTTAACATAAATTTTAAATTTATTTACTATTAGTTTTTATAATTTATTTTGAT TTACAGTGTGTTTGTGATTGTTTGTCTCTGAGAGTCCCTCTGCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
D90145	21 T C ---	---	---	ATTATCACTCTCAAAAATTTGGTGTGTGTTTAAGTACTTCTTATTATGAGCCCCCT/C/JGAGGA CCAGACATGTTATTATCAAGCCCCCTTATACCATCTAAT
EST14035 1a	59 T C ---	---	---	GCATTTTAAATTCACATTGAATCATTATTACTATTATGATGTTTACATAACAAATTCAGTATCAT ATG/C/TJGTAGATTTTCAGATGTAGGTCTGTCATCTAGCAGCACTTATCT
EST16668 5	71 C T ---	---	---	ACAGACTATCGCCAACTTATAATGCTTAACTTTATGATCAATAGTAAATTAACA/C/TJGAGATA TTCACACTTTATTATAAATAGGTTGTGTAGATGATTTTCCCAACTGTAGGTTAACAT
EST16904 7	57 C T ---	---	---	TTTTAAGTACCAGAGGCACTGCTGGACAGGATGAAACTGATACACCI/A/GJTTACTACTACTC TTCACCTTCAAACTGATTCCTCTAAAGACTTCTACTTAGCAAA
EST21863 9	49 A G ---	---	---	GGCTGTAAGTAGAATCAAGGTTAAGAACATTTTATGCACTTATTCACAAAACATTTACTGAGCATA CTAGGTGCTGGGA/G/JGTGACAGTGAGCAAAAACACAA
EST21885 6	80 G A ---	---	---	ATTTAGTGCAATGACAAAGCCCAA/A/GJAGAACAGAGGATCAATAAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTTAAACACAAGTATGGGAGT
EST22623 8a	26 A G ---	---	---	AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTACAG/A/GJAAATGTGGAAAAGATGGCTTTTAAACCC
EST22644 2	98 A G ---	---	---	CCTCATTATTAAAAAGACGGACATAAAAAT/AJTTACAAACAAAAACCCCAAGTCACATTTTCAG GAGTAAAACTAAAAGTCTGATATGAAAATATGGTGG
EST23587 1	31 T A ---	---	---	AAAGATCTGGCATTATTCACATCATCTAAATATTTTGTAAATCTTTTCCATGAGTATTTTTTCA TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACC/T/CJGAATAACCCATAGTTACAGAATTGG GTCTGTGTAACCTCAAT
EST24246 7	106 T C ---	---	---	TAGTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/A/GJCATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAAATATATAACCTCGTTC
EST24308 3	45 A G ---	---	---	CTTGAACCTTCTGGTCTGAAGTGTACGTCCGCTCAACCTCCCAAAATGATCGATTACAGGCATAAG CAGCC/G/JTGCCTGACCCACATTTCTTTATCCGATCTGTGTGAGACATTCAGGTTGTTTC
EST24435 6	73 G A ---	---	---	TATTGTTGCATTATCAAAATGGTTA/T/CJAGTTTCAATTAAACTGTAATTGATTCTCTATGTATAA ACAGCTTTGAAGTTGTAAATGTAGTTTCCATCGTTAGTTAATGCTACATT
EST25089 8	25 T C ---	---	---	

EST25476	33	G A	---	AATGATCTTTATTTCAGACCTGCTCCTAAAA[G/A]CTTTCTCCTCCTCTAAACCAACACACA AGAGGTCTCTTGCTGCTTTCCATGGACTGTGGCGCTGTGGACTTTGGACCTGGACCGTCTGCTGA
EST26183	70	T A	---	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACTTTGTAAAGATTGATCTCTAAATAAG ATT/AJACATTCTGGGGTACTGGGAGTTAGAACAAC
EST27231	28	T C	---	AGAAATAAGGTGCTACCAGAACTCATGT[C]GATAGCGCTTCCTTTTAGGCACATATTATAGCAATT CAGATGAAAGTTCTGTATACACACACACTGTGCTCTAACACAAACACGCGTGA
EST27816	26	T C	---	CAACTCAAGGTACAAGACAATTGCATT[C]TAAACATTGTTATAAATAAAAGGAACATCAGATCAAT CATTAAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588	78	A T	---	GTTTAATTGGGTATGTTCCACAGGCTGTACAGAAAGCATGTGCTCTCTGGGAGGTCTCAGGAA ACTTACAATCA/JTGGTAGAAGGCAAAAGAGAGCAGGCATCTCTCCATGACACAGCAGGAGG AACAGACAGAGGAGGGGAT
EST30226	25	A C	---	TACTCACACCGACATACATATCTCA/JCJGTAGAATTAGCTATACTGCATACTAACTTCACTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGCTAACTTAAACAAGACAGACTCACTTCCTTTGA G
EST30935	59	C G	---	AGCTATGGTAGAGCAAAATTCAGTGGTGGTAAATCAAGAACTCTAAAGTTTCAGTAGAGA[C/G]AGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515	25	G A	---	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCCTCTAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTTCTCACTTCCATTCCTATGAATACCTGGCAGCTGTTTATTCATGTTTATGTGAGTTCTATGC ATAAAAATCCAGTAAGA
EST33274	27	T C	---	TGCTTTGTTCCCTCCAAATCCTAAAA[T/C]GTGTGCTTCAAAGAAATTCGTGGAAAGGACTTTGAA TAGGAGTTGTACCATATTCAGTATTCTTGAATACAGGTTTCAGATACTATGGAGATGATACCATT GGACTAGGTA
EST33352	75	C G	---	TACACATTATTCAGAGACCACCTGACATGCATCTCCTCCGCAGAAATACATTCGTCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTATTTACTAAGAGAAATATCTCTGGTGCATATCTAGGGG
EST33424	126	A C	---	ATTTTCCACAGCAGAGTATATTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCGTACAGAAATGTTCAAAAGATTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTTGAATCCTCTT
EST33488	90	A G	---	CCTTTGGGGAGTTTTAAGCCAGAAATGTGACAAAGTCACCTACAGGAAGACTGGAATGTAGCCATAG TTGAACCTTAACATCGTCTATAG[A/G]ACCAATTTCCCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508	45	C T	---	AAAAACATGCTATTTGAACAAACTTTTTTATAAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---			AAAAACATGCTATTTGAACAAAACCTTTTATAAAGA[A/G]TAAGTTGACTGAAAGCAGGTTTTAAAT AACATCAACTCACAATGACTTTTGAAGCCAAATAA
EST33863 4	77 C T ---			ACAACATAGGACTGGTTATCTTGTTTGA AAAAATATATGTGCCACTTCCTATTTGTTTAAAAATGA TCATTTAA[C/T]TCTTTGAACCTACAGCCTGAATCCCC
EST34739 3	97 T A ---			GAAGTATCCTTCCCAGTGGCAGGAAGTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGAACCTCT[A/GGTGCTTACAACCTCAACTACTGCGAGAAATTTCT TGTTGTGCCTCATAAACA
EST34792 6b	104 A G ---			ACCTGACTGCTTTAAAAGCTCTTTGTAAGCTGACCGTAGCAGATCAGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GATTCAGGAATCTTAGTCCTATTACA AAGATTTTGTGCTGTG
EST34835 9b	93 T G ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGTGCTTCTGTT[G/GGCCCTTAAAAGAAACAGACAAATTTGTCTAAAGAT
EST34835 9a	82 G A ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTT[G/A]TGCTTTCTGGTGGCTTAAAGAAACAGACAAATTTGTCTAAAGAT
EST35230 0	93 G T ---			CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCTCAATAAATG CAAGACATGAGCATAAAAGAGGTTCTC[G/T]GCTTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---			TCCTTTCAAATTTTGATGAGGCATTTAATG[C/T]TATAAATTTCTGCTTAGGAATGTAATCTGCT ATATCTCAGAAAGTTGGGCATGTTGTTTCCATTTTACCTTAGTTCAGAACTTTTCAATTTTCATCT
EST35708 9	32 C T ---			CTGCCCCAAATTAACCTTTTAGGCAATGGAAA[C/T]AGACTTACTGTATGGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTTCCCTCTCTGAGGTGGCACCTTTCTCTGTTG ATGTCAAAGTGTGGCT
EST35747 9	51 C G ---			ATCCAGTGCAGAGTTGATGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---			TGGTCCATTATATAAACTGAGGGAACAACGGTGTGACATGGCAGACATTTATTTCAATGGAGA AGTTCCTCCCATGAAACCAAGA[C/A]CTTGCTCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAAGCCTGTGA
EST36301 4	93 C T ---			CACCTGTTTCATTTGGTTCAGTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTCTCAGCCTACAGC AGTCAGGAGGCAGCCATGGCCCTG[C/T]GCTGATGGAGCTTGTAAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---			GCCATCAGCCCAACAAAGACATGACTACCAACG[C/G]GGCCCCCTTGACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGCTTAGTCGT

EST36620 6	50 G A ---	---	GAC TTT ATT AGA TAA GGG GTT CGG CTAC CCTCA AAG CTCTC AGG ACTGG [G/A] GCTAG GGT TTTA AGG AAG GC TTA TTTAA TATGG GAA ATAA ATACA AAG GGC CAC ACC CGATG CAAA GACTTT
EST36690 0a	89 C G ---	---	CCTGTGATGTGCATGGGTCCCTGAGCAGTCGTACTTACTATCGTCAGACAGCTCACGTATGTTCAGGA AAGGAAGTCTGGGATTCCTA[C/G]AGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTCA
EST36729 9	62 C T ---	---	GAGACAGAAGCCCATCAGTTAAATGAGGTAGGCCTCTCCTCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTAGCTACCCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 A T ---	---	ACTGTCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATTATTTCTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	ATGATCGCTTATGTAAATTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---	---	GGTCTACTCTCTGCCAGGACGGTTGAACTCCTGAGCTCAAGTGACCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACACCTGGTCTTGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---	---	AATAGTCTATGGCTACGGCCCGTGGGATGTTAAAAATGGGATTTTAAATTAAAGATTGTGAACATG CAACCCAGCAAAATTTCTAGCTTATATTTGAAAGTCT[G/C]AGGAGAAAAAATGGGTCC
EST37284 2	93 G T ---	---	AAAAGACCTTTCTCAAGCAGTAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAAGAA GCTCTCTGGATAATGTCACCTCTAGGAA[G/T]AGTAAACAGGTGTTAAACCCCTGAGATAGCAACCCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90 A G ---	---	AGATGGGTCTTGCTAGCTTGCTCGGGCTGAACATAAGATATCCTCCTCAGCTCAGCTCCAGGTAGT TGGAACCTATAGTAGGAGTATCTA[G]CCCTGCCCTGCTAGAACTTCAAGTTTGATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACCTT[C/T]AAGGGTGAAGCATACC ATTCCATTTTAGTTGAAATATCCTTCACATAGCCAACACATTTTTTCAAGGCACTCTAGCTACTACA GGA
EST37376 8b	101 G C ---	---	GTGACATCATGTCTCTTCAATGOCCTTTCAATTAATAGTAGT[G/C]TGGGGCTGAGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGCTGTGCTCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 T C ---	---	GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAGT[G/C]TGGCGCTGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGCTGTGCTCTCAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63 T G ---	---	ACACACAAAAAATGGTGGCAGAAAAATCTGGAAAGATTCTAATAACCTCAATTCGTGAAAAACIT/G JAACATGCCTCAAAAAAGAGGGGAAAAAATTTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---	---	AAGACATAAATCTGCAATGAATCAGTTATGAATATTAACCTCTG/AJCTTCTCAGGAGTGACAC TAATCATGCTGCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAATCAATGACGTAGAA
EST37613 6	34 A G ---	---	CTAGGCATGGGCTTTACAGTCATTTATTTACCJAGJGTCATGAATTCATTAATAAACACACGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCAAAATCACCCCTGCGTTTCATGGATCTTCCATTCTAA
EST38025 4	56 T G ---	---	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATATCACTTAT/GJTTATCTCA ACAATCTTGAAGGTGGTATTATTTCCCGTCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57 C T ---	---	TCTACAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTCATGTCACTTA/CJTCGCATGG AAGAACGCTCTCTCTTTAATTCCTAATCTCTCTTCTGGGAAGACAGAACGTGCACAA
EST38420 6a	100 T C ---	---	TAAATCAAGGCTCTTTTCATTACCAAAACAAAACAAAAGGGAACAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTCACTGACTGACTGACTGCTGCTCCCTGCAGTGCCCATGGGTCCCGTGCCT TATTCACTCTCTCTCTCA
EST38950 5	25 T C ---	---	TTATTGCAAAAGTAAGCAGCGGGT/CJTGTCCTCGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAAGTATGGGATGAGAGAGGAACAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90 T C ---	---	TTTTTGTTACTCTGTAGCCAGTCATTAACTGAAGGTTTAAATATATATCATTTTATTTGGGATGAGATCA TAGCTTTACACAAATGCTATG/TJAAACAAGTTACTGAATAATTTTACCTCGTGGAGTTG
EST39331 1	70 G C ---	---	TCCTTCTGCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCATGGAAGGAAAGTA TGC/GCJGTGTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31 C A ---	---	GTCAACATTGACCTTACATAGTGCCTCTAGT/CJACCTATGAGGCCTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37 T C ---	---	TTCTAATAGCATGCCCTGTGACAGGGAACCTAAGCTC/TJTCAAAAAATACTGAAAACTAAATCTGTA AGATAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTCTCCAGAAAGGCTCAAGGTGTTTC AATAATCTGTGGGACTCA
EST40549 1	42 A G ---	---	TGTTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCACA/GJATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCACCAATTTCTCACTTTGAACCTAGCTCCCTGCAAGCACCTTCTA CCCTGCACCTTTGGGGAG
EST40579 1	81 A C ---	---	TGTGAATTACACATCAGTAAGGCAGTTTACAGAAATTTTCACTTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAA/AJGGAAGTGGAGACAGCGATTAAATACGGAACAAAGGCTTCCAGGAAG
EST40584 3	68 A G ---	---	TTGTATGTTGTAGGAATTTGGGAAGAAATATCTGTGAAGGAAATTTGCCACTGTAAATGCACACCC A/AJGTTCTGTACTCCCAATATCTCTATGTTTTAAGCT

EST51340	51 G A ---	---	GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---	---	CATGGGAGTATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAAACATAGAAGCTCAGAGCCAGATCCTTTATCCAACCTCTCGA T/CJTTTTCTTGGTCTCCAGTGAAGGAAAGCCCCATGATCTTCAAGCAGGGAAGCCCCCAGTGAGT AGCTG
K01506	63 T C ---	---	CTGAACCTCCAGCTGCCCTACAAACTCCATCTCAGCTTTTCTTCTCAGTTCATGTGAAAACACTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCTTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCATTCTCT TAGTAAAGTTTCCAACAATAGAAATTAATGACACTTTGGTAGCAGTAATATGGAGATTATCCTTTTC ATTGAGCCTTTTATCCT
L18877	69 T C ---	---	TGAGTCTGAGCAGCAGTTGCAGCCAGGCCAGTGGAGGAGTCTGGGCCAGTGCACCTTCCAAAGGCC CT/CJATCCATTAGTTCCACTGCCCTGTGTGACATGAGGCCCATTTCTCACTCTTTGAAAGAGAGCAG TCAGTATTGTAGTAGTGTCTTCTATTGGATGACTTTGAGATTATCTTTGTTTCTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---	---	GCTATTTTACATATCCCAAGCCCTTTAGGGCTACAGT/CJCTCTTCTCTGGACCCCTGTAGGGTGCCA TTTGGAGTTCACAGCCTAGAAGAAAGAAAGCTTTGGCCCTGTGTGGTCATAGGCCCTGTAACTCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTGAGACAAACCTGGGCAAT GT
L38517	137 G C ---	---	GGGTCCAGAAAGCCTCTCAGCCAGGAGGAGCTGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCTCTGCCATGAAGATACACCATTTGAGACTTGAAGTGGCAACACAGCGTCCGCCAC CQ[G/C]CGTGTGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G ---	---	ACTTGAGAAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGGACAGGGCAACAAATACAGTAGTAGTTCTTTTGTATTTTGTATATTTGJCGCCTGA AGATCATCCCGCAAGGCAGGCTGGAGTGCGGTGGCCCTGTGTGCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173 G A ---	---	CAAAGTTGTCTCTGCCCATGAGCACACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCACACCAACAAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAAATGTCT AAGGT

L48728b	111 T C ---		AAGTGAACAGAAAAAGCATGGATTGTTCTCTATAAAAGCACATAGTTATGTTACTGGTATCGT AAGAAAGCTGGAAGAAGAGCTCAAGTTTTTGTTTACTTTTCAGAAATCJGAAGAAGCTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAAGCTCATCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---		GCGCAGTCCAAAATACAAATTGGACAGAGATCTATATTGCCAGAACT[G/A]TTTATTTTCACC CCATCAAGTATAAGGTTACTGATTGATGGTCCTTTTATAAACATTGGTATATTTCCATTTCATGCCAA AGCAAAAGAAAGTAAAAGCTAA
M19169	113 T C ---		TAGGGATCTGTGCAGGCCATTTCGACACGCCACGCCACTCCACCCCCTGTAGTGTCTCCACCCCC TGGACTGTTGGCCCCACCCCTCGGGAGGCTCCCATGTGCTGT[C/J]GCCAAGACAGACAGAG AAGGCTGCAGGAGTCTTTTGTTCAGCAGGGCGCTCCGCCCTCTCTCTCTCTCTCTCTTAATA GC
M21539	114 T G ---		TCACCTCGTTCCACAGCTCCACCTGGATCTTCTCATCAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCCATGATGATCCCGACAGCAAAAT[J/G]GTTTCTTTCTTGAGGCTG CCATGCTGCCACTGTCCAGGTGAGACTGAGCAAGGAAGTCTCAGCTGTACCGGCCCTTTCAGAGCT TCTCTTTGGGTGC
M26041c	173 A G ---		CCTAGCATTATTTCTGGCCCCAATTAICATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCTTTGAATATTTCCCTGACTTC CTGATTTTTTCTTTTCTCAAGTGTACCTACTAAG[A/G]GATGCCTGGAGTAAGCCACCCAGCTACC TAATCCTCAGTAA
M26041b	157 A G ---		CCTAGCATTATTTCTGGCCCCAATTAICATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCTTTGAATATTTCCCTGACTTC CTGATTTTTTCTTTTCTCA[J/G]GTGTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATCCTCAGTAA
M26041a	45 C G ---		CCTAGCATTATTTCTGGCCCCAATTAICATATCCCTTTTCTCCTCTCTCTCTCTCTCTCACCTCT TCTTCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCTTTGAATATTTCCCTGAG TTCCTGATTTTTTCTTTTCTCAAGTGTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATCCTCAGTAA
M63967	57 G C ---		TAGGCGAGCTGTGAGGGAGGCCAGTCCAGTCCAGCAATCCACAACCCCTTGAC[G/C]AATGCT TGCCAAAGCTGTTTTAAAGCCCAAGAACACCCCTTCTTTTGTCCAAATTAACCTCTTAGAAGAAACCCCA CAATAAAGCAATTCATC
M81695	34 G A ---		ACTTACTTACCCTCACTGTGAGGCTGACGGGGA[G/A]GAACCACTGCACCACCGAGAGAGGCTGGG ATGGGCTGCTTCTGCTTTGGGAGAAACGCTTGTGGGAAGGGGCCCTTGTCTTGTCAAGGTTCT CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCCAAAAGGACTTGACTTGCAATTTCTACC T

U08641d	166 C T ---	---	CTCCTCCTTTATTTACAGCATGGAGGGTTAAATGGAGGATCTCCTTTTCTGTGACAAAACATCTTTC ACAACTTACCTTGTTAAGACAAATTTAAAAAAGATCTTTTCAACAACCTTACCTTGTTAAGACAAAAT TATTTCCAGGCTATTTAATACGTACTTTAGC/TJTGGAATATTCTATGTCAATGATTTTAAAGCTA TGAAATACAATGGGGGA
U09607	39 T C ---	---	GAGGCTTATGAGGGTCTCTACTTCAGGAACACCCCA/TGJGACATTGCAITTTGGGGGGCTCCCG TGGCTGTAGAATAGCCTGTGGCTTTGCAATTTGTTAAGGTTCAAGACAGATGGCATATGTGTGAG TGGGGCTCTCTGAGTCTGCGCCCAAGAAAGCAAGAACCAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82 T C ---	---	GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATTCCAAAGGCCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC/TJACATCTGCCCCCTTCCAGGCCCTTCCCAAGCCCCCTCTCTTGTCTTC ATTCATTCAACAAAATTTGGC
U10694	20 C G ---	---	GTGACATGAGGCCCATCTTJG/GGCTCTGTGTTGAAGAGAGCAATCAGTGTCTCAGTGCGCAGTGG GTGGAAGTGAGCACACTGTATGTCTCTGCTGTTCTTGTCTATTTGGGTGATTTGGAGATTATCCTT GCTCCCTTTTGAATTTGTTCAATGTCTTTAATGGTCAGTTAATGAACCTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162 T C ---	---	AAAAGGAAGTCTGGTTCAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGACAAAGTTGTTTAAAC CTCTTTGTTGAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCAAAGAGATT/CJTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTACCTTCAGCA
U15555	187 T C ---	---	TTTCTGCCACTTTCACCTGGTTTAAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTTGAAGAATTAAATAGCAATGCTGAACATCAGGAATTGTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG/TJGTTGGTCTCATAC CTCATATGCAGGATTCAATCA
U17077	122 T C ---	---	TCCAATTATGGTCCCCAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTACAGAACGTCCTGACAGACTGAGCGATGACACCACAT/CJTGTGTTGG ACATTTAAATTCACCTGCTGTAATAGGAGGAAGCTTTCTTTTCTGGGAAACCAACTGTCTCTTGG AATTA
U18543	58 T C ---	---	GCACATGCAGAATAGACTCAGCCTATGTCCTGATTCCAGCTGGGTAGTTCTAGAACTTT/CJAGAAG CTCCATCTTTTAAATGTTTATTGTTATGTCCTCCCTCCCGGCTTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACCGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACTTCC AAGGCTTAGTAGAGAGGCC

U25975b	164 C A ---	---	TCAC TGCTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAACAAATGACTATTCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAGAC/C/AAGATATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143 C G ---	---	TCAC TGCTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAACAAATGACTATTCTCTG AAGACAAC/C/G/AAGAGAAAAATTGCAAAAAGACAAATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61 A G ---	---	CAGGAGAGGTTATTCACAACCTCACCAACTAGTATCAATTTAGGGGTGTGACACACCA/A/GJTT TTGAGTGTACTGTGCCTGGTTGATTTTAAAGTAGTTCTATTTCTATCCCTTAAAGAAATTT GCATGAAACTAGGCTTCTGTAAATCAATATCCCAACATTTCTGCAATGGCAGCATTCGCCACCAACAAAA TCC
U28413	29 C T ---	---	ATTCTGACAGCTAAATTAGCCCTAAATG/C/TGGGTAATATTTTCTCATGTTTTAAATGAGGTT AATATTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCTTGATCC CAGATGTTGTGGCCTGGAAAGCCCTCATTGCTACAGTACAAGTAACACAAGTCGTTGTACCTCAGTT G
U30884c	89 A G ---	---	TAGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTGGGACCTGCCGTATAATCTGTT CTTCTATCCACGTTAGCCA/A/GJTTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAAGT GCTGTCA
U30884a	34 A G ---	---	TAGGGTAGCATTTAAGATTCAGGAGTCATTAGC/A/GJGTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATCCACGTTAGCCAATTTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAAGT GCTGTCA
U31216b	78 A G ---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCAATGAGACGGCTGCAACCAAACA GCCGTCAATCA/A/GJCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGACCCCTTTACAACGTAGAGGAGGAGGATGCCAGCCGATTCCGCTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70 G A ---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCAATGAGACGGCTGCAACCAAACA GCC/GJTCATCAAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGACCCCTTTACAACGTAGAGGAGGAGGATGCCAGCCGATTCCGCTTAGCCCGCC TGGTAGCCCTTCCAT

U31416c	76	G A ---	---	AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAQ[A]CCACAAATCTGGTGCTCTCTCTTGCCTTACAATGTCTAGTCCCCACTGCGTCTCT GGAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTTCACTTGACCCCTGCCCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68	C T ---	---	AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGCGTGAGTCTTCATCTTAGGGCATCGCTC IC/TTCCTCACGCCACAAATCTGGTGCTCTCTCTTGTCTTACAAATGTCTAGGTCCCCACTGCGTCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTTCACTTGACCCCTGCCCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78	C T ---	---	ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGCTTATGCTCCCACTCACATTGTTCTCTCC AGACCGCAGG[C/T]TCCCCAGCCTCAGTTGCTGGAGCTGTACATGACTGCATCCTGCTGCCAGG GCTGCAAGCAAGGCTTCTCTATCTGGGGACGCTGCTGAGAGAGGCGGAGGCGCGCAGAAC ATGCCAGGTGTCC
U37690	54	A G ---	---	GACCACGCTGAAACCCACCCCGCTGTGCTGACCATGGGCCCTGAGCGTCTTATGJCCCCGAAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCCTGGCGCAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTCTT
V00540	39	T C ---	---	TGAAACCGTTTCAACATGGAATGATCTGTATTGACTAAT/CACACACAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCTCTATAACCCCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106	A T ---	---	TCAAGAAGGTGACTGCCCTTGTATGATGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTTTAAATATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCTAGAATTGGATTCACTCTGTTTTTTCATGTCTCTCTT GTAAACCCTGAGATCATCAG
X52011b	148	C T ---	---	AGGAAGATCCCACCGACCCCTTCTGGCCTAATCCTTTAGATTAGGTACATTACATTAACTTTAGGA ACCCAGACCGAAAGTTGCTGAAGGGAAGGAGACACATTACAAAGAAAGTTGCGAAATTTGCG AAATCTGTTGTGCA[C/T]GCTCAAATGAAACGCCCTTTCGGCTTTTATTTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118	A C ---	---	AGGAAGATCCCACCGACCCCTTCTGGCCTAATCCTTTAGATTAGGTACATTACATTAACTTTAGGA ACCCAGACCGAAAGTTGCTGAAGGGAAGGAGACACATTACAAAGAA[C/G]TTTGGGAAATTT GCGAAATCTGTTGTGACGCTCAATGAAACGCCCTTTCGGCTTTTATTTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT

X87344	34 C T	---	---	CATCCCAAGGCACCTGGTGGTACTCTGCTCTCTGCTGCTACTGACCCAGAGCCCTCTGCTGTGCACTGC AAGCTGTGCTACTCAGGCCCAAGGGGACTCTCTGTTCCATTCTCCCCACAGACCTGTCAAGAG AAGCATGACAAACAATAATCATTTACCGACTTTAGTGTCTTTT
X87838	179 G T	---	---	GGTGGGCTGGTATCTCAGAAAGTGCCTGACACACTAACCAAGCTGAGTTTCTATGGGAACAATTGA AGTAAACTTTTGTCTGGTCTTTTGGTCGAGGAGTAACAATACAAATGGATTGGGAGTGACTC AAGAAAGTGAAGAATGCACAAGAATGGATCACAAGATGGAAATTTA/GTJCAAACCCCTAGCCTTGCTT GTTAAAT
Z14138	81 A G	---	---	GTCTGCTGCCTACACAGGGGCCCTGTACAGTGAATGGTGCCATTTTCGAAGGAGCAGCAGTGTGA CCTCCTGTGACCC/GJTGAAATGTGCTCCCAAGCGGCCCTGTGTGTGTGACATGTGAAGCTATTGTGAT ATGCACCAGGTCTCAAGGTTCTCATTTCTCAGGTGAAGTGAATCTAAGGCAGGATTTGAGAGTTCACA GAAGGAT
Z18859	191 A C	---	---	TAATGCTCACCATTCTCAGGTATAAGTTCTATAAACAGGCTTGGAACTCTGGGTAAITTAACAAACAGA AAATTATAGTCAATATACCATGACATGAAGATGAATCCATTCTTTGGAGATGGAGTATACATGACT GCAACTGTATTCATACGTTCTTTTCAAAGTGGGATAGCTATTGCAGCTTAAGAGC/GCJGAGGTTTC CAGTACTGGTTTCCAA
Z23091	159 G A	---	---	AGAACTGACAGATGTGGCTCGAGGGGAATCCAGACCCGCTGCTGTCTCTCCCTCCCTCCCTCC CACTCCTCCTCTCTCTCTCTCTCTCTCACTGCCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTG CTCTGTGCTCTCTCAATCTCA/GJGGCCCGCAACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTGAAA CTGAGCTTGACGTTTG
11595b	125 A G	---	---	GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAAGTTATTTTATCAAA GTGTGGTTTCTGCAAGGCGAGGTTTGAAACCTGACCTAGTTGTGCTCCAGGACCTA/GJGCGTGC TCACCTACCTTGCTTTGTGTGAAGGAGTGGTTTCCATGACTGTTTAAAGTGACAAAGTGCCATGG ATATCTACACCGTCAACGACTAGATTGTCTCAATGTCTTGCTTGCTTGCGAC
11595	125 A G	---	---	GTTGGCATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAAGTTATTTTATCAAA GTGTGGTTTCTGCAAGGCGAGGTTTGAAACCTGACCTAGTTGTGCTCCAGGACCTA/GJGCGTGC TCACCTACCTTGCTTTGTGTGAAGGAGTGGTTTCCATGACTGTTTAAAGTGACAAAGTGCCATGG ATATCTACACCGTCAACGACTAGATTGTCTCAATGTCTTGCTTGCTTGCGAC
1241	131 G T	---	---	TATATCACATTAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTTGAA TGCTCTTGCTCTTCAATAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCAGCTTGT JGCGAGGAGTGTTAGGATGAAGAGAGAGAGATTAAAGGAGATCAGGAAGAAAGTAGCAATGGGA ATGAAATAAGGAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAG

1282	130 C T	---	GTGGATCACCACTACAGTCTAATTCAGATGTTTTCATTACCCCTAAAGAAATCTTGTACCCATTAGCAATTTCTCCTGCTGCTCCTCAGCCCTACTCTTTATCGCTATAGATTTGCCQCTACTTGACATATCATACATGGAGCCATACATATGTGTGCCCTTCATGATGGCTTCTTTCACACTGAGAATAATGTTTTCAAGGT
6810	68 C T	---	AGTATCACACATACCTTAATATATTAGATATACACAATAATAAAATCACTCCCTACCTTGAAAACTTTA/C/JAGAAAGCATTTTAAATTTACAACACAAAGCTCAACGAACCTACAATAAGTCTAGTAGTCTGTTACGTGCCAAGGATAAGGCTGAACAATAAATTAACCCCTTAAAAATGCTATGAACAAGTACAAATTTCTTTTGGTCTGCAGAGCAATGACCCTAAGAAATATTTTTAAAGGC
6817	118 A C	---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTGCTTTTGTAAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGGTAAC/A/CJGTGGATACCCCTG TGTGCTCTACTGGCCTCCAAAGGCATTGAGGGGATCAAAAGATGTTGGACACCTTGTGTTCAAATC TTGTTGAGGTGGCCTGTGCAGATCGGCTTTTGGTTGGTGTCTTAG
6819b	212 C	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACITTTAATGGAAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGTCCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACTTTTGTGTTTCTATATGACACCTAATATCCA
6819a	166 G T	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACITTTAATGGAAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGTCCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACTTTTGTGTTTCTATATGACACCTAATATCCA
681xx	39 A G	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATTG/JTTATACTATGGCACCATTGGGACA CAGATTATATATGTCAGACACCAAGATGTCCTTTAAGATATGCAGCAAGCACAATCTGTCTATGGT TTAACAAAAGAAATGAACGTCTAGG
6972b	149 G T	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAAGGAATGGTACCAGTTCCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGCTGGACTCTTTTGGTTGGTAACTATTGATTATG CACAAATTCAGAG/GTCCCTGTTATTGGTCTATTCAGAGATTCAACTCTTCTCTGGTTTAGICTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122 A G	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAAGGAATGGTACCAGTTCCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGCTGGACTCTTTTGGTTGGTAA/GJCTATTGATTA TTGCCACAATTCAGAGCCTGTTATTGGTCTATTCAGAGATTCAACTCTTCTCTGGTTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

7598k	210 A C ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTCCCT CAATGCAG[AC]
7598j	208 A T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTCCCT CAATGC[AT]GA
7598i	192 G T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTT CCTCAATGCAGA
7598h	144 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[CT]ATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTT CCTCAATGCAGA
7598g	142 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGAT[CT]CCATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTT CCTCAATGCAGA
7598f	120 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTGGAGAAATGAAATATTTCTTGAGGATGCCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTT CCTCAATGCAGA
7598e	83 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[CT]CAGATTTTACCTGGAGAAATGAAATATTTCTTGAGGATGCCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTT CCTCAATGCAGA
7598d	77 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCC[CT]GCTAACAGATTTTACCTGGAGAAATGAAATATTTCTTGAGGATGCCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTT CCTCAATGCAGA

7598c	56 A G ---	---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCC/A/GJAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGAGAGAAATGAAATTTATTTCTTGAGGATGCGTT TTAATATTTGATCCCATATGTGAGAGATTTTCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGAGAGAAATGAAATTTATTTCTTGAGGATGCGTT TTAATATTTGATCCCATATGTGAGAGATTTTCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	---	AAAGGTAATCAAAGTCCCTCTATAAATTJ/GJGATTTACAAAAGACACCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACAGATTTTACCTTGAGAGAAATGAAATTTATTTCTTGAGGATGCGTT TTAATATTTGATCCCATATGTGAGAGATTTTCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTGCCAGCTCTCCTGTA ATACCTTAATGAATGGGTGATGCTCTATCTCAAGGTCCCAATATJ/CCTTGAGGTTCT
7998b	94 A C ---	---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTGCCAGCTCTCCTGTA ATACCTTAATGAATGGGTGATGCTCTATCTCAAGGTCCCAATATACCTTGAGGTTCT
7998a	75 A T ---	---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTTCAGACATCTGCCAGCTCTCCTGTA ATACCTTAATGAATGGGTGATGCTCTATCTCAAGGTCCCAATATACCTTGAGGTTCT
8071	119 A G ---	---	---	AAATACAGAAATTTATTTAGAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAATGGGTCCCAATAAATGGAATTTTAGGGCAACAAAGTCTAAAGGCC/A/GJCAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCAATTTTGGCATTTGTTAATCACTGAATC TGGGTTTCTCTGAATCCACACAGAGCATGCACACACATTTTATCAT
8467b	93 C T ---	---	---	AAGGCTTCTCTAAACATCAGTCTACGGAGAACTGGGAAATCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA/C/TGGTCACTCCGAACTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAGGAAAAAATCTG
8467a	70 A G ---	---	---	AAGGCTTCTCTAAACATCAGTCTACGGAGAACTGGGAAATCTGGATATTTGGCTTATCACTT TG/A/GJCGCAAAATCCACTTTGCTGTAAACGGTCACTCCGAACTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAGGAAAAAATCTG
8498	84 C T ---	---	---	AGGGTTCAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG/C/JAATACTTCAATTAATCGAAAAAGAAAAAATTTGCTTTAAGGAAAAAA AATCCAGTTTTAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCTCAATACAGAACCCAGGAATGTAATTTCTCACTCAG

WI-18562	29 G A ---			CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTCATTACATTT TAGCATTAAATCAGAAACGA
WI-18618	51 A C ---			ATAGCAGACTTTTAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAACI[C/J]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAAGTATAATTGTTAAACCCACAGTGCTCGCACAGTTC AC
WI-18683	22 C T ---			TAAGCTGTTCAGGACTGGACTC[C/J]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAATAAATTTCTCTCCCAAGCCTGCCTGCAGT
WI-18520	75 G A ---			GACTTTGGTGATTTAATTGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAATACTACTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCCTCTCCGTGAGAC
WI-18563	94 A G ---			AAATAAGTTTATTGGCACACAGCCCAAGCCAGTGGATGACACATTTGCCACGGCTCATCTTGCAA TACAATAGCAGGGTCACTAATGTGACI[G/A]GACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69 T A ---			GTCCTATTTCAATTTAGCTAGACCCATTTCATCTGTTTAAATGGCTACATTTGTTTTTCATTGTGAGAC T[A/J]GTGCCATAATTTTAAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCAG
WI-18723f	94 G A ---			AACCTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAACCAA[G/A]ATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71 T C ---			AACCTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGCTGTAGATTTTGAAAG TGGT[C/J]AACAGGTACATAGGTAACCAAAGTATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96 A G ---			AACCTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTGACTGCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAACCAAAGTATAGCTTATTGGTGAATCTTCATCCT
WI-18819	44 G A ---			TTTATTACAATTTAGGTGGCACATAAATAACAAAGCTTCTGA[G/A]ACAGGAGGTAAACATTCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA
WI-18715	76 G A ---			TTATTCACAAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGAGCCCTCCAGTGAAGGGTATTTTTTAATAAAAAAATAA TGGAGCTACAACCAACCCG
WI-18535	107 G A ---			GTAATAAAGTTTATTGGCACAGCCAGCTGTTTCATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCAAC CTTCTGTGGTCCCCCGTG
D17525	107 C T ---			AGAGTGGTGCAGAACACAGGCCGAAATCCAGGCTCTATCACTTACTAGTTTTTCAGTTCTGGCAGGTGAC TTCATCTCTTCGAACCTTCAGTTCTTCATAGATGGAAG[C/J]TGCTATACCTTACCTACCTGGTAAAA GTCTGATGAGGAAAAGATTAACTAATAGATGCATAGACCTTAACAGAGTGCATAGCATACACTGTTT TCAATAATGCACCTTAGCAGAGGTGATGTCTCTACCAGGCAGCAAG

DWU-133c	313	A G ---	---	TAATGGCCACTGCCCTTATTATTACAAAACAGAAATGTCTCATGACCTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTGTTAAATGAATATGTCAGTTTGAATTTTAAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---	TAATGGCCACTGCCCTTATTATTACAAAACAGAAATGTCTCATGACCTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTGTTAAATGAATATGTCAGTTTGAATTTTAAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---	TAATGGCCACTGCCCTTATTATTACAAAACAGAAATGTCTCATGACCTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTGTTAAATGAATATGTCAGTTTGAATTTTAAATAGTAA[C/T TTCCAAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---	ATGAGATCCTTTAAATCTTCATGAACGTTTGTGTGGTGACCTCTACGTCAAACATGAAGTG TGTTCCCTTCAGTGATCTGGGAAGATTTCTAC[C/T]GACCACAGTTCTTCAGCTTCCATTTCCGCC CCTCATTTATCCCTCAACCCCGAGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGGAG AAACAAATAAGACCATAAAGGAAAGGATTCATGTGGAATATAAAGAT
DWU-387	169	G T ---	---	GTGTATAAATGCAACTGTTGATTTCCTCAACATGCTGCTCACAATTTCTATCCCAATCTTTCTGAA GATGAAGAGTTTAGTTTAAACTGCCTGCCAACAAGTTCACTTCATATATAAAGCATTATTTTAA CTCTTTTGAGGTGAATATAATTTATATTACAATG[G/T]AAAGCTTCTTTAACTAAGTATTTTCA GGTCTTCACCAAGTATCAAGTAATAACACAATGAAGTGTCAATTATTCAA
DWU-447b	172	--- ---	---	ATTTTAGTGTCTTTGCGTTAAANAATCATTGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT GGGCTGTGCCATTTAAATCACTGTAATTAATTAGTTTGATTAGAGCACAAGCTTAGCTAATCAA CCATTATTTTCAATTTGTTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTGTTAG GCCTTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-447	85	A G ---	---	ATTTTAGTGTCTTTGCGTTAAANAATCATTGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT GGGCTGTGCCATTTAA/GJATCACTGTAATTAATTAGTTTGATTAGAGCACAAGCTTAGCTAAT CAACCATTATTTTCAATTTGTTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTG TTAGGCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-476	63	C G ---	---	GTAAATTCAGTTTTTCCAGTTCCCTCTTTTGTGCTGCTCTCAATTAGCGTTTAAAGGTGAG[C/G]AT AAATCAACTGTCCATCAGGTGAGGTGCTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67 A T ---	---	---	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGCCCATACAGAAAATCTATCACCATACAAAAATTA A/TTCGAGTATTTATGTTTAAAGCACAGGTGTACCGAAACTGTGAAAAGTCTGAATTTATGGGTT CTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTGACTTTGAGCTTTAAACTTTTAA
DWU-512	131 A G ---	---	---	AAATCCAGGCATTCGAATCTGTTTTCATGATTTATAGAGGGTTACACAAAGTGCCACTATTAA AGAGCTCCACAGTGAAGATGGAGAAGGTGAACCTGCTTTGAATATCCAGATGTTGTTGGTC[AG] TGCGTATGGCAGTGAGCAGGTATGTTGCTTTTGCTTGCACTGAAATTAATTTGCTATCAAGAGC AACTATGAACGGTTTTTATCAAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	---	AACTGCATATAGATAATTATCCAGGATGTTGGCTCATTTTTCAGCTGTTTCTACTGTTTGT ATATACAGTTTTTGAACCATATGATTGA/C/AAGAAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATTTCTGCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAATTCAGTCTCTGATTGC
DWU-59	94 C T ---	---	---	CATTTCTTTGTAAAGGTAATGGACTCAAGGGGAAGAAACATGCTGAGAATGGAAAGTCTACCGG CCCTTCTTTGTGAACGTCACATTGGC/C/TGAGCCGTTGTCAGTCCAGGTGCCAGACTGTTTTTG GTAGTTGTTTTAACTCCAAGGTGTTTTACTTCTGATAGCCGGTGATTTCCCTCTAGCAGACATG CCACACGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68 C ---	---	---	CTTGATCATGGGTGGAATTTTGTGATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCGAGGCTCTGGATCAGAAAAAAGGCA
WI-18856b	63 C T ---	---	---	CACACTGGCATCTAGGCTTCGCCCTGCTGAGAGGAGAGCCAGGTCCCTCTGGAGAA[C/T]G CTGCGTCCCGAGCCACACCGGCTTTGCACACACAGGCTGTTGAGCAGGAGGTGGTGAAGAGT AGCTGTAGACCCAAAGCAACCCAGCCCTGGGACCTCGGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGTCATCCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA/AGGAATGAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAACAGAGATTTCTCAAGGGCAAAGTGGCTTCT A
WI-18036b	97 T A ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAAATACAAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAATTTCTTTTCATAA/T/AGTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTT/C/JAACTTCTAGAAAATACAAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAATTTCTTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	---	TGTAAGGTGACTTCTATAAGCTTCTTAAACTGTCAAACCTTTCATTTACTGAGATTATTTTCAGGCCAAT GTGTC/TJTGTTGGGCTGAGATTGATTATCAGCTGGGTAAAGTTAACCTGTTCTCTGTTCA

WI-18063	105	GA	---			AGGCTTTAAACTGATAACAAATTTGCCCTTTAATCAGATACAAAAGCTGTCACACTTTTCATTCTCCTTC
					---	CCATGTTTTCTGATTTTGATGTAAACTTTAAATTTTGTTGATTCCTTTAAACAATATACACTGTAGCTGCA
WI-18078	86	AT	---			AGTTGAAAGATCAGAGAGGTTATGGTTGGTGAGTAGCTGAACCTCAGATTCAAAACCTGGTCCAGTGTG
					---	TTGTTTTTTCAGCATCAGATTTGTCCTAGCCAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	TC	---			CCAAAGCTCACTCAGTATTTAATCATCTGCTAAATTCATCTCTTTTGTAAATCCATCAGACACTGTGGT
					---	TTTCATCTCTAGAAGTTTGAGCTTTTCJGGGCTTTTATACCTTCCATATCTCAACTTGTTAAGC
WI-18119	38	TC	---			GCAATCTGTAACAGTTTGGTAGTGGTATTACAGAGGATTCJTTGTAAATGGATTGGAGTACTTAC
					---	CACTATTTTCATCTGCTCTGAAATAGTTCACTAACCAACTACTGACAACAGTTTAAATTTGGTTCTT
WI-18142	66	TG	---			TTCAAGATAATTACAAATGGAGGGGACCAATAATTCACCTTTTAAATCGAAATAATCTATATAC
					---	T/GJCCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAGAGGAAAA
WI-18178	68	TC	---			GCATAGGGTTGAGGGGTGTACAAGAGGGAGAACCCAGATTCACTGTCATCTGATAGCAGGGCATACAG
					---	GTCJCGGCGGGATGGACACAGACAGACACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35	GT	---			TCAATCTGAAAACCTTGCTGAAGCCAGCATGGGGTG/JGGGGAGGTGATTATGGCTGGGGAAGATG
					---	GGCACTCACCGACAGCAGCATCTAGCACCAAGTACAGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	GA	---			ACAGATGTCAGTTGTTGAATTTGGCCCAATTAAGTATGGGGCTTTCTTGTAAAAAGTCAATCCAAA
					---	AGGCTTGGCAAGAGTTTGCTATACAACGGAGGGACAGAGAAACATGA/JCTGGGGAGTAGGCTCT
					---	GACAGAAGGTGGGCTGTC
WI-18261	26	GA	---			GATTTGAAGGGATTGCTTTATTTAAC/JATGAAAGCGTGATAGAGGAACTGTTTAAGATAAACAA
					---	CTTATAAATACTCCCAATTTGTAGAAGTGAAAGATTG
WI-18268	88	CT	---			TAGAGGGGAAAAGGAGGTGGGCTGCCTGGGCOCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAGC
					---	TTCTTACTTCCCCCATAGATTC/JCTGACAATGTGCTGCAGAAAGCCTCCAACTGGAAC
WI-18299f	107	CA	---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACCTGGTTGCCAATTTTTT
					---	ATCTATTTGGGTCTGAGAAATCCACAATTTTGA/JGAAATCTTTTGCCAAATATTGACATATTCGT
					---	CAG
WI-18299e	101	AG	---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACCTGGTTGCCAATTTTTT
					---	ATCTATTTTG/JG/JGCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATATTGACATATTCGT
					---	CAG
WI-18299d	77	GA	---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACCTGGTTGCCAATTTTTT
					---	TG/JATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATATTGACATATTCGT
					---	CAG
WI-18299c	67	TG	---			

WI-18298b	52	GA	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGCTCTAGATCATTAACCTTG[G/A]TTTGCCCAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAATCTTTTGCCCAATTTATGACATATTCTG CAG
WI-18299a	48	CT	---			TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGCTCTAGATCATTAACCTTG[G/A]TTTGCCCAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAATCTTTTGCCCAATTTATGACATATTCTG CAG
WI-18307	76	GA	---			TCAACTTGATACCAAGTTTAGCAGCAAGAGGATACTTCCTTAGAGACTTTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TTGCTATGTAAAGCATCCACGATGGTTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72	CT	---			TTTGGTATGAAATCTTCTCTGACATTTACCAATCATCACTTAACTCGGGGGTGGGGTACTGATT TATC[C/T]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48	TC	---			ATGAAAGTCACTTCAATCATAGGGTCAAGAGAAAGAAATGTTTTTCAGAT[C/T]TAAATCTATGAAAA GGTGTATCTGCTTGCAATTTAAGAAACAACACAAAGTCA
WI-18395	77	GC	---			TCCTGACATGATCTGTGAAATAACGTGATTGTGGTTGAAATTCCTGTGAAAAATTTGAAGAATAAATTG ATTATTCAAG[G/C]TTGTCATGGTTTATACATATCTCTCTTCTTAAATGCAAAAGCTATG
WI-18398	82	GT	---			TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAGAAAAAACAACACTCAAGGGTT[G/T] GATAACATTGCCAGTATAACCAATAATTCAAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18396	21	CA	---			CTCGTTGGTATTCTCTCATCC[C/A]TTCTCTTTTCGCTCTTTCTAAATTAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACTTTAACTTATCAACTTGACAAAAGTC AATGAAAA
WI-18409a	20	CA	---			AAGATGGGAAAGAGGAAATC[C/A]TTTCTTACTAGAGATTTTTTTCCTTTAATCCTTTTCAAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAGCTCTGGGGCCAGAGGCCCCCAAGTGCTA
WI-18442	62	CT	---			AAAAGGAAAAAGAAAGGATGGAGTAAGAGAGAGAGACAGAGAGGAAACAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAAAGGAAACACAAAGAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18452	38	GA	---			TTGATGTTAATACTGTCTATTCTGGAGATCGGCTAAAATG/AJAAAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTAAACAAGTAAGACATATATCAACCCTCATATTTTCCAAACCA
WI-18489	102	AC	---			ATATAAGCTGGAGACTGTGGAGGTGAGAGGAGTGGGGACTAGCTGTGAAAGAGAGATGTAGC AGTAGTAAAGATGAAGACTGCAAGGATTCAAACA[C/G]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
EST5b	93	A	---			CTGGTGGGAGGAAACAAATTTGGGTATATTTCATACAAATGGAAAACTCTTCAGAAATAAGAAAGGAA CAACCACTGAATCACACAACATGGACAATCTCAAATCATTATGCTGATGGAAAGAAACCATTC TAAGAATACACAGTACAT

EST5	93 A ---	---	CTGGTGGGAGGAAACAAATTGTGGTATATTCATAAATGGAAAACTCTTCAGAAATAAGAAAGGAA CAACCACTGAATCACACAACATGGACAAATCTCAATCATATTGCTGATGGAAAGAAACCATTCAT TAAGAAATACACAGTACAT
EST6	48 C ---	---	TTAGCTACTTTTCAGAATTGAAGGAGAAATGCAATTATGTGACTGAACCGACCTTTTCTAAAGCTCT GAACAAGCTTTCTCTTTTGCACAAGACAAAGCAAGCCACATTTTGCAATTAGACAGAT
EST8	158 A ---	---	GGACAGGAACCTCTATTCCGCTGTGTGACAGCGGCTGATGACTGAGGCCCCAGGGATACTGGGOC CTCTCTCAGGGGCGTCTCCAGGACCCAGAGCTGTCTCTTGGATTCCCTAGAGCTGTGCGGCCA GATAGCTGTCTCTGAGTTGCAAGCACGATGGAGATTGGACACTGTGTGCTTTTGGTGGGT
WI- 18740c	104 GT ---	---	TCCTCATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAAAATTAGTAACAACGACCTAGAAAAAGT GAGAACAAATCTCATTTACCATCATGTATC/GJAGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C G ---	---	TCCTCATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAAAATTAGTAACAACGACCTAGAAAAAGT GAGAACAAATCTCATTTACCATCATGTATC/GJAGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 CT ---	---	CCAAAGTCTCTCTGTCCTATAAAGAGTTTGGGATGGGAGAGAATCCAGACCCTTTGGGGCA GCCAGGCCCTTGCCCTTCATTTTACAGAGGTAGCACAAC/JTGATTCACAACACAAACCCCTTCGCC TTTTAAATGATTCTGTCTAATGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTGTTTCTCTT TGAAGCAATGACAAGCACTTACTTTCACGGTGGTTTTGTTTTCTTAT
WI-18746	114 GA ---	---	GCAGCAGCTGAAGTCTCTTTCTCTCTCTCGGGTGAAGAATCAAGATACCTTTGCGTGGATCA AGCTTGCTGACTTGACCGTTTTATATTACTTTTGTAATAATCTTG/AJTCCACATTTCTACTTCAGCT TTGGATGTGGTTACCG
WI-19112	212 GA ---	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCCCTGGTTACGGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAACACAGATCAGTAGTGTCTATCTCATGACAACCAAGAAACCGACGACAAA TCTTTTGCAGATTTCTCTAGTGGCTTAGAAGATGGCTTTAAGAAACACCGGTGATATCTTTGAG GGTGACAAGGC/GAJTCTCTTCAAACAGTTCATACCAACTGCTTTGCTCTAG
WI-19092	232 AC ---	---	TGGTGGCTGGCTAGCTAGTTTCTACAGAACATAATTTGCCCTCTATAGAAGGCTATTCTTAGATCATGT CTCAATGGAACACTCTCTTTCTTAGCCTTACTTGAATCTTGCTATAATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGTCTTTGTATTAACCTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTTC/AC/ATGATTAGCCGTGTAAC
WI-19057	175 GA ---	---	CCCATTATTATAGGCCAGTGATGTCTCAAGAGTAGAGGAGCGTCTACTGGTCTTTCAACTCCTTCA GTCTTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGATTTGTACGTCCAGGCAOCCGACGACTG TCTTCATGCAGGAACACAGTGCAGATGCCACAGCTC/GAJTCTCTTCTATCTTGGTTTTGCCACA

WI-20103	168 C T ---	---	TGGGACTTCCAACCTCAGAGGATGTGGGAATCCAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGAGTCATGGGTCAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAAGCTGGTCTCCCAAC/TTTCACTTCTGCTCAAAGCTTCTTGAAGGAGC TGGTTGACTTCAACTTGTAGAGCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ---	---	GCCTACCCATTTGCACATATACATATGACACACCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGTAGGACAAGAAATGGA[G/A]TTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATCTTACCCGTTTTTCACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ---	---	TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAAGACGT TTTAGTCTTTTAACTGAGTTTAAAAAATAAACAATGCAATTTTAA[G/A]ACACTGTTTTTGA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ---	---	GTCCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATAATGGCATGGAGGAGGCAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAA[G/A]AAAGGGAGTTTCCACGCGCAGGTGGTGAGC TGC
WI-20613b	156 A C ---	---	GTCCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATAATGGCATGGAGGAGGCAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAA[G/A]AAAGGGAGTTTCCACGCGCAGGTGGTGAGC TGC
WI-19984	47 A G ---	---	CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAATAA[G/A]TATAACATTAGAAAA GCAAAATTTCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAATGAAGGCAGTTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ---	---	GCCAGTTGGAATATGGCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTTCATCAGGCAATA ATTGTTTCTTGGAACTCTGCACCGACTGTCCATGCTCTGTGGGACTTACACATTCAGTTTGACAG[T/C]TGAAAAACCAACTGGAGCTGCTTTCCAAAGATGTTCTGTCTTCAATAGGAATTCATG TTATTTCTTCTTGCCCTTAAGCTCTTATATCTTTCAAAATGACCTAAGCTGA
WI-18846a	49 G A ---	---	GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCCT[G/A]AAAGCTGGGAGCGT GGGCTCAGCAGGGCTGTGCACCTCCCATCCCGTAAGACCTCCTCCCTCAGCAGGCCCAACATG GCCAGACTCCTT
WI-18959	123 G A ---	---	AGCAGTGGCCTTATTGCATCCCAACCCAGCCTCTTGACAGGCTGCCTCCCTTGTGGCAGCAACGGC ACAGCTAATTTCTACTCAGTGCTTTTAAAGTAAATGGTCGAGAAAGAGGCACCT[G/A]GGAAGCCG TCCTGGCGCCTGGCAGTCCGTGGGACGGGATGGTTCTGGCTTTTGAATCTCAAGGAGCGAGCAT GTCGTGGACACACACAGACTATTTTAGATTTCTTTTGCCCTTTGCAACC

WI-20146	31 T C ---	---	---	TGAGTCTTCTGTAATTCATTGAGCAGTTAGCT/CJCATTTGAGATAAAGTCAAAATGCCAAACACTAG CTCTGTATTATCCCATCATTAAGCTGTAAGCCCTCATTTGAATGTGTAATTCATACAGGC
WI-18922	74 G A ---	---	---	TAGGAATTGGTTTACGCTGAGGCAATTAGACACTTTTGGAGATGGCATAACCTGTCTACCTGGAC TTAAGC/GAJTCTGGCTGTAATTCACAGTGTCTTTTCTCTGCTACTGTATCCAGGTTCCCTCCAGAG GAGCCACCACTCTC
WI-18763b	53 A G ---	---	---	TTTCTGTGTGTGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA/JGJTATTTAGAATG TACCATATTTTGTAAATTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18763a	38 A G ---	---	---	TTTCTGTGTGTGGGTCAACCGTACAATGGTGTGGGA/JGJTACGATGATGTGAATTTAGAATG TACCATATTTTGTAAATTATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18771b	75 G A ---	---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAGATGTTGGG AACAGAA/GJA/AAATAAACTGAGTTTAAAGGGGACTTAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---	---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG/JGJAGATGTT GGGAACAGAGAAATAAACTGAGTTTAAAGGGGACTTAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C ---	---	---	GGGAAAATTTGAGACGCAATACCAATAGTATTTGGTCTTGGTGTATGAAATTTCTGAG GCC/T/CJGATTTAAATCTTTCATTGTATGTGATTTCCCTTTAGGTATATTGGCTAAGTGAAACTT GTCA
WI-18742b	51 C T ---	---	---	ACAAAGTCTGTAGCCCCCTCACCTTTCTGTTTTCACCTTTGCCAATGTA/CJTATCGGGTTTGGTTT TCTTGTATTATTTAAACGGTTGTGGTTTCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94 C T ---	---	---	GTGTGTCCAAAAATGGGGTCTGCTGCTACCTTGACCCCTTCCCTTTCTCTGCTTCTCTCATCA TCATTTCCCAACAACATCCTCTGCCA/CJTACACAACAAACGTAAGTTTCA TTTGGGCAAAAAATTGA GC
WI-19970b	167 G A ---	---	---	TATAAGCCGAGTCACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCCAOC GGCCCCGGCAGTCAGTCAGTCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTACTCGGGGACC AGCAAAGGCCCTTCTACTGGGTTGGTCAAAAG/GJATAGTCACCTTGGCTGTGCATCCACAGAGGA TGTGTTCAACCAAGAAATCTTTAAACGACTGACCTTCTTAAAAACAGA
WI-19970a	126 T C ---	---	---	TATAAGCCGAGTCACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCCAOC GGCCCCGGCAGTCAGTCAGTCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTACTGCGGGG ACCAGCAAGGCCCTTCTACTGGGTTGGTCAAAAGGTAGTCACCTTGGCTGTGCATCCACAGAGGAT GTTGTTCAACCAAGAAATCTTTAAACGACTGACCTTCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGTGCTACTGCTGACATTACGGCAGAGCAAGGCTGCTGCAGCCTCCCTGGCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCGAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAAAT/ GJACATAGTATCTCTCTCAAGACGTGGGGGAAATTATCTCATATC
WI-19067c	153 G C ---	---	TATTGCTGTGCTACTGCTGACATTACGGCAGAGCAAGGCTGCTGCAGCCTCCCTGGCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCGJGJAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATCTCTCTCAAGACGTGGGGGAAATTATCTCATATC
WI-19067b	151 T C ---	---	TATTGCTGTGCTACTGCTGACATTACGGCAGAGCAAGGCTGCTGCAGCCTCCCTGGCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCGJGJAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATCTCTCTCAAGACGTGGGGGAAATTATCTCATATC
WI-19067a	57 G C ---	---	TATTGCTGTGCTACTGCTGACATTACGGCAGAGCAAGGCTGCTGCAGCCTCCJGJCTGGCTG TGCATATCCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTT CTCTGGGCTCTAGGCTCGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATCTCTCTCAAGACGTGGGGGAAATTATCTCATATC
WI-19106	247 T C ---	---	TTAATCCAGCCCTACCCCTGTGTTAGTTATTTAGGACAGCTCAAGCAGCTAAAAGTGGCTAATTC AATTTATGGGTATAGTGCCAAATAGCACATCTCCACAGTTAAAGACATGATGATCAATGAAAGT GCTGTTTGTCTTTGAGAAAGAAATAATGTTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGCCATAGCCTATAATTGGTTAGAACCTCTATTTTAAT/CJTG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTTATTATGTAGCTGAAACAAA AATGCCAGAAAGGATAATATTGATTCCTCACATCTTTAACTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAACJAGJTGTTAAATTAATTCACAATAAAGTTCTACAGTTAATTATGTGCATA TTAAACAATAGCCCTGGTTCAATTCCTTCCTTAATAAAATTAAGTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTAAAGTGAAGGATGGATGTTTCATAATACATAAA GTTCTGTAAATTACAACTAAATATTATGCCCTCTCTCACAGTCAAAGGAACTGGGTGGTTGGT TTTTGTTGCTTTTTAGATTTATTGTCCTAGTGGGATGAGTTTTAAATGCCACAAGACATAAATTTA AAATAAATAAATTTGGGAAAGGTAAJGJACAGTAGCCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCAGAAACTGGAATAAGCCTTCGAAAGAAATGTCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTTTGTGCTGATTTGACCTTGTATTCAAGTTAACTGTTCCC CTTGGTATTTGTTTAATACCCTGTACATATCTTTAGTTCAAJCTCTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAAAGACGTGCTGTGGGAAGACAAGTCTGGGCTTG

WI-19042	193 A C ---			TTTGTCAAGTTGCTCTCGCAATGCCCTCAGTAGCATCTCAGTGTGTGTGAAGTTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTGAACCTTTGTGCTTCAAGACATTTGGTAGAGTCCAAACAG ACACAAATTTATAGTGCAGACAGAACTTCAGCATTGTAAATTTATGTAAATAGCTTAACCA/JC/JGGCTG TGTTAGATTGTATTAACTATCTCTTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---			ATTGGCCCTGTACAGTTTGGCTATTATTAATTCATTAAACACTACAGGTGTGAATGGTTAAAA TGTAGGCCCTCCAGTTCAATTTTCAGTTATTTCTGAGTGTGCAGACAGCTATTTCCGACTGTATTAAAT GTAACCTTATTAAATGAATCAGAAGCAGTAGACAGATTTGGTGCAATACAAATATTGTGATGCATT TATCTT/JC/JATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGACT
WI-18851	90 T A ---			GCTTCAATTGGCGATTGATTGAGTGCACCAATGTAAACAGGGTTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCTTATTGTATTCTT/JA/JGTAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT/JC/JGGGGGTAGCCATTGTGCAGTATGGCCCGGGGAAACTTGCCAACTTCGTGTGACG GTGCTGTGT
WI-18821a	68 C T ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A/C/JTAGAGGCTGGGGGTAGCCATTGTGCAGTATGGCCCGGGGAAACTTGCCAACTTCGTGTGACG GTGCTGTGT
WI-19021a	20 C G ---			ACTCCTCTGCTGTCCATC/JG/JACTGTCTCTTTGAACCAAGGAAAGTCACAGAGTTTAAAGAGAA GCAATTTAAACATCCTGAAATCGGGAACAAGGGTTTATCTAATAAAGTGTCTCTTCCATCACGTTG CTACCTTACCCACACTTCCCTCTGATTTGGGTGAGGACGTGGCATCTACTTACGTACGTGGCATAAC ACATCGTGTGAGCCCATGTATGCTGGGTAGAGCAAGTAGOCTCCCTGTC
WI-18908	70 G C ---			TGGAAATCCCTTCACTGTGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG/JC/JTAGGGAACATTCATCCTTGAGTCAAAAAATCTCAATTTCTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---			CACGGTTCTCTGCATGTTACAGAGCGGCTTCTGGTCTAGCCACGCCCTGTATGACCGGCAATA TCCCCAAAGCTTTGGGTCTCAAGTCATGCCQGAATTTAGATGCTGTGTCATTTTCTGGAGAGGGTC CCCTCCCTTACGAACACAJA/JA/AACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGTGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---			CACGGTTCTCTGCATGTTACAGAGCGGCTTCTGGTCTAGCCACG/C/JCCTGTATGACCGGCA ATATCCCCAAAGCTTTGGGTCTCAAGTCATGCCQGAATTTAGATGCTGTGTCATTTTCTGGAGAGGG GTCCCTCCCTTACGAACACAJA/JA/AACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGTGTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---			TTGAGGAGGTGGGTGAAGTGTCTCTTGGCAGGGATTTGTGACACTGCAATTCCTGGGCTGTGTCTCT/ C/JGGGCTCTCTGGAACCTTGACCGTGGATACAGGGCCATGTGCCATTTGGGTCTCTGGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---	---	AGCCTGTGGCTTATGTCAACCAACAGAGGGGTCTCTGAGAAGTCTGGCTGCCCTGGGATGCCCCCTGCC CCCTCTGGAAGGCTCTGACAGATGACTGGCTGGGAAGCAGAGTCTTGTCTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCCTTCTGTGGCCACACGCACTACGGCTTCTCTCC AGATGTGCTTTGCCCTGAGCACACAGATCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A ---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATATGACATGGTAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTATTAACGAAGTTCAAAGATTAGAAATACATCTGTGT CTGAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCTCA/C/AJCTCAACACTATTGAC TTTGGGGCTGGATAGTCTCTGTGTGGGGTTTGTCTGTGCACTGTAG
WI-19016a	161 C T ---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATATGACATGGTAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTATTAACGAAGTTCAAAGATTAGAAATACATCTGTGT CTGAAACCTTAGATACATAGCCG/C/JTGTATACAGAGGTTCTCAACCTCAACACTATTGAC TTTGGGGCTGGATAGTCTCTGTGTGGGGTTTGTCTGTGCACTGTAG
WI-20096	21 T C ---	---	GGTTTGGGGCATTATTCTGTGATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCGCC ACCCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	TGGGGCAATTTTAAACAAACGAGGCAAAATATACATATACCTGAATATAAGGTAACCTCAAGCCATG AGTAAAGATTAAAGGCAAGTTACTTTATTTTGAACAAGAGTGBCATAAGCAACTCAGTGTGCCCC CTTAGGGTGGGAGCTCTTCC/C/AJCTACCACCTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	TGGGGCAATTTTAAACAAACGAGGCAAAATATACATATACCTGAATATAAGGTAACCTCAAGC CATGAGTAAAGATTAAAGGCAAGTTACTTTATTTTGAACAAGGAAGTGGCATAAGCAACTCAGTGT GCCCTTAGGGTGGGAGCTCTTCCCTACCACCTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	TCCTCAGCTGTCTCCTTGTCTTGGGGTCTGTGTTCACGGCCCTCCAGGCATGTTTCTTCAT TTAGTAGGAACAAGGCCAAAGAACATACAAGCCAGCTCTAGAGGCTCCA/GA/JTCAGAA CTGGACCTTTAACTACAAGGAATCTTGGATGAATATTTTACGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACTCAGGCCATCTTCTCCCAATGTCTCCCGGGGG
WI-20860	224 G A ---	---	CTCTCCCTAAGGAGCCTTGGCCTTGAGCCCAATTCAGAGGATGGAAGTCAAGACAATGAGT GGAGCCTCATGCCCTCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTATCTCTCTCT CCCAAGTCTGTACACTTGGCAAGCAGAGTGTGGCAGACCCAGCCTTGAGAGCTCTTGTAGACC GGAAGGAAGGGCGCTCATTTG/JAGGTGATGGCTTCTGTGCTCTCTGCTT
WI-19359a	39 T C ---	---	GACGTGGACAAAGGAGGTTAAATGAATACTTTGTTTGT/JC/JCATGTTCAAAAAAGAGTATTAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTTGGGCAATGCTGCAATATCTCTGGCCCTCAAGTGGGAGGCCACGTG GGAACAAGGCTCAGAAAAACAAAGGACATGCAGCCTCCCTGAGCCAGTTCCT

WI-19766b	93 A G ---				TGGCCTCAATGACTGGTACATTGGAGAGCTGTGACGACGATCCTTTTCTGTGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTC/GAGACAAACAGAAAGGACACACCAAGCCTGAAACCCCTCGGACAAACAGAGATTACAGCTGAGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTCACCTCCTTCAACCTCCTACCAACCAAGCTCCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---				TGGCCTCAATGACTGGTACATTGGAGAGCT/GAGTGCAGCAGCATCCTTTTCTGTGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTCAGACAAACAGAAAGGACACACCAAGCCTGAAACCCCTCGGACAAACAGAGATTACAGCTGAGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTCACCTCCTTCAACCTCCTACCAACCAAGCTCCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---				CTCCTCTGTTTGGCTTTGCATTTGTGGATTGGAAAAACCACTTGGAAAGGGACTTTCTCTGCAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGA/C/GJAAAGCTTAGAAAGGAAGTAAATTCCTTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCACGGCTTATTAATCCAGGCAGTTGGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---				CTCCTCTGTTTGGCTTTGCATTTGTGGATTGGAAAAACCACTTGGAAAGGGACTTT/GJTCCTGCAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGCTTAGAAAGGAAGTAAATTCCTTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCACGGCTTATTAATCCAGGCAGTTGGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---				GGGCTTAAATCCCTCTGTTTGGGACTGTCTCTCCAGTTTACAGCAAGGATCGCACCCCTTTTCCATAACCCCTTGTACATTGGAAAGAGCACACCTTGATACAGATGGTCCGTGAAGTCTTTTAAACGGACAAAGGTAAATCACAGCTAACAAACGTGATGTGGCTCACACGTAAACCAACACCTCTTTTTCAGAACAGAGAGCGTTAAAGTAAAGGGCA/C/GJTTCCAGAGTAACACTGCTA
WI-20679	82 T C ---				TGTTTGAATAAAAATTCATGGTCTTAAATGAACTGTATGTTACTTTCTTTAGAATATCCTTTTTCATTTAAATAATTT/CJTTAAACACTCTATGTGTTCAACCTCTGTTTAACTAAGATATGGGTTTTGGAAAGGCCACAAAGTCACAGCTCCATGAAGTGGCGAATTGGTCTGTTTGGAAAGCTCTCAGGGTGTCTCCAGAAA
WI-19909a	29 T C ---				CCAGAAATAAAGCCTGAATATCTCTTTT/CJTTAAAAATAAATTTTCTTTCTTTGCTCTTCCAAATAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATATAACACTACCTAGGCGGGTTTTTCTCTTATAACCTTGTCTGTACTGTGGAAATCAACTAA
WI-20341	221 G C ---				TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTTGTAATAGTCTTAGGGGCATGAGACATTAGGAAGGCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAGCTACTGCTCCCATTTGTTAGCAGGAGGAGGAAAGTATCTGGGGTCTCTGGCAGCAAAAGCGTGTGTAATATTTGGGTGACGTATGCATCCCCCATGCATTGGTTTTC/JATGTCTCCAGTGAGCTGTGGGCAAGTCT

WI-20113	60 T C ---	---	---	TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGTTCTGGAA AACAGTAAAGCAAATACCACAAATTAGGAGGAATTATTTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATTCAGCAATAAATCTTATTCATTAACAGGTAGATAATGTGACAA GCTTTAAATATAGTTAAGTACAGTTGATCTCGTTATTCATGAGTTCCGTATT
WI-20895	107 G C ---	---	---	TGATGGCAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGCAGTGCAGCGTGTGGC CACTTCCACAGCAGGAGAACACTTGACTTTCATTAAAGCAAAGCTTTACTCTGTTACTTTTCTCTC CCACATAGTTTAAACCCAAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCTCAGGAA TATACTGGTACTATAGGCAACAGATGCA
WI-20721	72 T C ---	---	---	CCTGCAATCACAAAGTGGAACTAGTTGATATTTTGAATCATACTTGATTTAACCCACCTTCAGAAA TTCATATTC/AAACACTAGCAACTCTCTTTATCAGA
WI-19415c	161 A G ---	---	---	CTGGATTTTAATATTTCTGGCCTAATAACCAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTTCGAAGATTCCTTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAA GTCATGAGACCCCTTAGCTGATCTCATGAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCTCTG
WI-19348c	103 C T ---	---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGATGGTGGGTAGCAAGTACGATGGCCATGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCAATGCGGTGAGCTGCTCTCCAGGCTCATATGGATGTCTCT CGAGGTTGCACAGGGAACCTGCTCTGCTGTAGAAGCTTCTCC
WI-19348b	98 G A ---	---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGATGGTGGGTAGCAAGTACGATGGCCATGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCAATGCGGTGAGCTGCTCTCCAGGCTCATATGGATGTCTCT CGAGGTTGCACAGGGAACCTGCTCTGCTGTAGAAGCTTCTCC
WI-19635	98 A T ---	---	---	ATTAGTTCGTGTTGGGCCACATTCAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAAACAATG TTAAAGGTACAGTAAATAACAGTATTATATATCTTATTGTAGCACGGCTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCACGCTGACTGCATGCAGATATGTGTGCTGAAAGAACTTTTGCTT T
WI-19641a	46 A G ---	---	---	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAGTATGTTATATAGTCTCATGTTT TTAATTTATGAATAACGTCTGATTCATTTGATTTTGTATTTACAGAAGATGTACAGGCTATCTCATTC AGTTATTAATAATGGATCAGAGTAGTAAGTCAAGATAAGTGCATAATGTGTTTAAATTTTAA AATACTCAGATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52 C A ---	---	---	ATATAGAGTACCATCCATGTTTCAAGCATGGCTGGACACATTATCCCCCTTC/AGGGTAAACCAG GACTATTGCATGAGCATTCCTTAAATAGTATTTTGTATGGACACAAAGTTTTCATGTCTATTA
WI-19673b	180 C T ---	---	---	TCTGCCATGATCACATTGTGATGAAGAAATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTGCTCT TACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTTGCATCACCACCTGTAATCTAATAGT GAAAGGGCAATGATGTCTCAGTATCACTGTGAAACATTTTCTGCTGTGGACCAGCTGAAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCAAAAAAACACAGCCC

WI-19673a	35	G A ---	---		TCTGCCATGATCACATTGTGATGAAGAACATGATG[A]JTCACATAGTAGGTAACTTTCTGTGTCTATTG CCTTACTCTCAGTAGGTGCTAGTGGATTACCTACCCCTGCTTTTGATCACCACCTGTAATCTAAT AGTGAAGAAGGCAATGATGTCTCAGTATCAGTGTGAACAATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCACACAGTCAAAAAACACAGCCC
WI-19724	35	A G ---	---		TTTATTTGGGAACAACAAAGGATTGTAATTTGGGTAA[A/G]CTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTGGTTTCTCTT
WI-19307	196	T C ---	---		TOCTCTCCCCAACTAGATGGTATTGATCAGTCTGCCACAAATGGTACCCCTTCAGCAAGAAGCTG CAAGCCCTCTTGGATTGCTTCATGAGAAATGGTGGCTTGGGATGGAGTGACATTCCTTGTCTGT GGTGAAGTGAAGAAGAAACAGGCAATGATTCCATAGAGGCCCTTAAAGAGACCCG[T/C]TGG AATGGCCATGGTCTAATTTGGTGTGAATAAACTAACCTCTTTGGCTG
WI-19269	85	A T ---	---		CTTCCCTCATCCCTCTTCCACACACCATCCCGAACAAGTCTCCAGGATTCCTGCCACTGGC CATTTTGGAGTGTCTC[A/T]TTGGGTAGCAATGTGGAAACCAACAGGCCCTTTGTGGAGAAATGG AGGGGTTGAGGGAGTCCAGGAGGGCTTATTGAGGGCTTTTGCCACTTGCTCATAGGCGAGCTCG ATCTCTCATCATCTGGACAGGTGAAGCGAATCTTCCCGCGTAGGCA
WI-19946	122	C T ---	---		CAATGGACTGAATGAGTGTGCTGGTGGGTGGGCGACACACACCTTCAATACAGCTCAAGGTG CTTCCAGTTTATAGAAACAGAAATCTGCATCTCAGCTGAGACGACAGAGAGGTC[T/CT]TCCCTG ACCCAGACGCACCTCAGGAGCCAGTCTGGTTTCAAACTGCATTTAACCTGCGGCGAGAGTTCAAC CGTAGGCATCTTTAATAAATACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G A ---	---		CACAGCATGGTGAATAATAGCATCAGATTGAATGAAAAGTTTGTAAATGCAACCATAAATAATTATA ATAAATATACATCAAGTAACCTTACAGCACACATTTTATAGGCCAAGGTTGGATCTGTCTGGACCT CAATGTG[A/CT]CTCGGAGAAAGCAGCCACGTTAGCAGCAGATACCTTACAGCTGTCTACTCAA GTGATGGCAACAGAAAGCTTCTGAACCTCCTCTGGGAGGTAGCTGACAAG
WI-19076	40	G A ---	---		TTGGTTGGATACTTGTCTGGAATAAAAGCAGTTTAAIG[A/G]ATTCAAAATACCTTTTAAAAA GTATCTAGCACAAAGATTTTCTGTAACTAGATTATGTTGTAACCTTTTCTAAATCTTGTAGGAG TGCGGTTGTTAAGAACTAGAGCTTATCCTATTCCAAATCTATCTGCGCTCCTGAAAAACTGCAGA AAGGCACCTGAAAGCTGTTTCTTAAGATATGGATTCTTTTATCTT
WI-20218	26	T C ---	---		CCACACTCTGTTTTTAAAGCTA[T/C]AGGACAGAGCAGAGATGGAACCTGAAAAACAGGGTAG AAAATAACATAAATTGGAGGGAACAGTGGGATGAGAAAGAAATGACAACAGCCACATGTGCCCCA GTCAAAATACCTTTAGTCCCTGACGAGAAAGATGCCAACCAAGTCTCTATCTGCTGGGATCTCGC ATGGATGACAGGAGAAAAA
WI-20295g	154	T G ---	---		CAACCTTTTGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAAATATCTCAGGCTTGAATGGGAGGGCTGGGCTCTACCCCTTCTTCTTCCCA TCCAGTCTATTGCCAGAT[G/C]CAGAGAAAGCGGGAGGCCAGCTCTCCAGCATAGCCACTGTGG GTGCGCTTCACCTTCTGTCGACTCCTCATGCTGGGACTTGCTTTGCGGG

WI-20361a	192	G A ---	---	CTGGGAGTGTGACCTAAGTGACATTTTTTTAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGG CTTATGCAAGATGACAGAATATGTGAAATCTGATTGTCCAGAGTTACAGTCTGCACTGCCAAGCTA CAACAGTCCACAGCTGAGAGGTTCCCTATACTTCTACTGTGACAAATTTAGCG/AJATCCTTC AATGGGAAATTCCTAACTACACGAGACAATGGGTCCTACAGTAGGCCCG
WI-20572	75	A G ---	---	GAGCCAAACCCAAACAAAATAAAACAGAACTCTTTTGTAACATAAGTCATACCTACTTTCTCT TCAGAAATT/GJTCATAAAACATCATCTTTACAAACATGGAGAGCGAGGTAGGCCATAATTTGTTCA AATTCATCTTTCTCAAAATTTAAATTTGTTTAAATCCCAAGGTGCTATTGAATCTTCAAAAATA AACTGCCTATCAGGTATCATACCTGCAATGCTTCTAATATCTCTTGATTAT
WI-20588	133	G A ---	---	CATGACAAAAGACAAAGATCAAGGAGTAACATAAATTATAAGTTGAATAAATAGTATACAGCAATC TTCACTTTTTAAGAAAATGTGAGATCCTTTGTGGTTTTTATTCCTTAAGTACAAAATGCTAAACI G/A/GGAGCCGAGCTCTTCGCAATTCAGG
WI-20593	79	A G ---	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAAACTCCAGTCTTTTTCAGTCTGTG CTGTACTTCAG/A/GJTTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAGGAACCTCAGGATGTTGTAGGAAGGGGAGTGGATGCCAGGCTTCACCAGACTAT CCAGAAGCCATTCCATGGGTATTGGTCTGCATAGTGTGAGACACTGAGCT
WI-19765	57	T C ---	---	TTCTTTGCCAAGCCTGTTCTCAAGTTATTCAGAACTGGGTGTATACCTTGTCTCTCA/TCTATGTATCT TGTCCTGCTGTCTTTAGGTTAGCAAGGTGTATGAATACTTTAAGTTTTGTTGTTCTTTCTCCTCGT GGTATCAGTGAATACTGATCTATTCTCTGGCTAGGGTCAATTTACAAAATTGCCATGGAAGTGAAGC AAAAGGCCACAGTGGGATAAAATCACTCACCATCGAGGCCACCAAGTATT
WI-19066f	239	A G ---	---	TGACAAGGGAGAGAGAGGAAATTCCTACTCATTCGCAAGGAAATCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGAACTGG CATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTCCATATTCGCGATGCTCAATTACAGT ACCATTGCAGGCAAACTTTTCTTAAAGCCCTTCACTA/GJGTTTCTTTTA
WI-19066g	184	C T ---	---	TGACAAGGGAGAGAGAGGAAATTCCTACTCATTCGCAAGGAAATCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGAACTGG CATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTCCATATTCGCGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGCCCTTCACTAGTTTCTTTTA
WI-19066f	148	T C ---	---	TGACAAGGGAGAGAGAGGAAATTCCTACTCATTCGCAAGGAAATCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGAACTGG CATATGTTCTTGCGT/CJTGGTCAACCTGTAGCTGAATTAATCTCCATATTCGCGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGCCCTTCACTAGTTTCTTTTA

WI-19086a	147	G C ---	---	TGACAAAGGAGAGAAAGGAAATTTCTACTCATTTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAATGG CATATGTTCTTGCG/CJTGGTCAACCTGTAGCTGAATTAAGTTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCTTCACAGTTTCTTTTA
WI-19086c	100	G A ---	---	TGACAAAGGAGAGAGAAATTTCTACTCATTTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATC/GJTCCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAAGTTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCTTCACAGTTTCTTTTA
WI-19086b	87	C T ---	---	TGACAAAGGAGAGAGAAATTTCTACTCATTTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGA/CJTCTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAAGTTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCTTCACAGTTTCTTTTA
WI-19086a	72	C T ---	---	TGACAAAGGAGAGAGAAATTTCTACTCATTTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA/CJTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAAGTTCTCCATATTCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCTTCACAGTTTCTTTTA
WI-20860	105	G C ---	---	TTTACAGCGAGTTTTTCCCGTCTCAATAAGTATGAATGTAAATAGATTAGGGTGAAAGAAATGTG TGCTAAATAAAATCTCCCTTTTGAATGTATATTG/GCJTAAATAAGGGAAGCATTAAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTGATTCCTACTGTTTCTGTACAAGATAGAACA AAGCTATCCACCGCGCCCAAAAATCTGTTTAAACAACACTATGTTTAAAGA
WI-18768	120	C T ---	---	CTGCTGCAGCTTCTCTTGCGCTGCTCCAGATGCGGCTCTCTGCGAGCCTCCCTCAGTCTTCC TCCACCGCTCTTCTCTTCCAGCCTGCTGCTGATGTCACCTTGCTG/CJTTCGCTCATCGCC TTGAAAGCTCTGAA
WI-19087	37	A G ---	---	TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATGTA/GJTATTTAACTTCTAGTTGCTTGTCTTG GTCTTCTTCCAATGATGCTTACTAGAAAGCAATCAGACACAATAGAGAAGCCTTTTCCATAAA GTGTAATTTTAATGGCTGCAAAACCGCAACCTGTAACTGCCCCCTTTAAATGGCATGACAAGGTGTGC AGTGGGCCCCATCCAGCATGTGTGTGCTCTATCTTGTCATCTACCTGCTCC
WI-18790	49	A T ---	---	GAAAGCCAGAGATTAGCCCCGATTCCGCATCTGTCAACCAGGACAGAA/TGTCATGGACAAGGGA TGAGCTTTACAAGATGATGCACCTTTGGAGATCAGAAAATTCATATTTAAGCAAAAGTGATACAACA CAGTGATTTGGGAATGCT
WI-18987	35	G A ---	---	AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCTG/GJGTGGCCAAAGCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGATCTGTGCTAGGCTGACAGGATTACAGAAAGACACAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTGCACAGCCCCCTACACTCAAGGCTGAGAGGCTCAGGAA AGTCA

WI-18919	26 C	---	---	TGGATGAAACACACAGGGATTCCGGAGCTGGCCAGACCCCATTTTATACCTTCTACCTTTCTCTACAGTG TTGTTTGTGTGTTGTTTATTTTATACCTTTGGCCATACACAGAGCTAGATTGGCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G A	---	---	CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38 G C	---	---	CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23 T G	---	---	CTTCTGGTCAAGGCTTTGGACAT/GJCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170 G A	---	---	TCAGAACGACATGGCATCTGCTTCTGCTGCTTGGTTGGTTGTGTACCTTTTACGAGACCTGAAAT TTAGAAATGGCCAGTCTGCCAGAGTGAGTGAGTAAATCTCTCTTTCAGGTAAAGATAGGCTATCTC AACACTGCTGAGTGATTCTAAACATATCAACCA[G/A]TAGCATTAACCCATTTTATTTCTCTGTCTCT AGTGTCTGAAGATGCTCACCAAGTTTCTGTGACAGTAAGGCAGCATGCT
WI-19212	46 T A	---	---	CCAAGTTGCATCCATGTTGATTTTCTGATGAGAGTAGAGTGACAGT/AJGTTTCAGAACCCAAATGT CCTCAGGTAGTTGGAGCATCTCTATGAGATGGGATTATGCAGATGGCTATGGAAATGCAGCTGC ATAATTAAACACATTATCAAGTCTCTTACAATTTATTTCCGCAGCATGTCTGCTAGTAGACCCCA ATGGGGAGAGAAATGCCTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210 G C	---	---	CTGTTGAAGGCTTCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAAGCACACATTGGATG GCAGCATGGGTTTCTCCCATTTTATGGGCATGAATAATATGTGTTTGAATTAAGGAACAAGCATTATT CCTTTGCCAACAGCCTCACTTAAGAGGCTTTTGTGCTGAGTCAAGCAACACTTGCCTGCTCTGCGC CTTGGAG[G/C]TGCAATTGACCTGCTCTCACTGGTAAGGTGACTTGTGTGGC
WI-20014b	214 T C	---	---	TTGAAATCCAGTCTCTGGCCCCCAGGAGGCTGTGCACCATAGATGTCTCTCTACTGGGTC GTTCTGGCTTTTGTAGAAACTTGGTCTGAGTGTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTACAGAGCAATGTTCTTGATTTCTGAACTGGAACTGAACAGTTTGCCTTCTCCTAGTCACC AAGCATACTT[G/C]CTGGCTCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198 T C	---	---	GTCTCCCAGAGTCTCTGCAACCCAGCCCTGTCTGCTGCTGTAAGGGATACAGAGAGCTCCCCG TCTCTGCATCCCTTCCAGGGGGTGCCCTTAGTTTGGACATGCTGGTAGCAGGACTCAGGGCGTG CACGGTGAAGATGAGGCCCAAGCTCATCACACAGGGGCCATCCTTCTCAATACAGCC[T/C]G CCCTTGCAGTCCCTATTTCAAAATAAAATTAGTGTGCTCTTGGCTGTCTGT
WI-19135	20 G A	---	---	CAGTTACCTGCTTGGCTC[G/A]AAAGTGTCAATTTGTAATTTTAGTATTAACTCTGTAAAAGT GTCTGTAGGTACGTTTATATATAGGACAGACCAAAATCAACCTATCAAAAGCTTCAAAAAC TTGGGAAAGGGTGGATTAAGTACAAGCACATTTGGCTTACAGTAAATGAAGTATTTTATTAACT GCTTTTGGCCATAAATGCTGATATTACTGGAACCTAGCCAGCTTCAAC

WI-19236	54	G A ---	---		TACACAGAGGGTGGCACTTGGACTCTGAGGGTGGGTGTGGAAGGGGAAAGG/GA/GATGGAGAC CTGCTCCCGAGCTCTTCTGTGACCGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGAGGT CACCTTACCCTTTTTCATAGGGGAAGAGTGTACACTCTCTGGCTATCTCAGGGGAATGGGGAAG AATCTTTCAAGGGCAAGAACTCGTGGAGGATGCTGTGTATGTAATACT
WI-19144	222	G C ---	---		GTGCCAGTCTTCAGAAAGCAAGGACTGCCCTTCATTACGCCCTGCTGACCTCCAGCCCTTCTAAGG CTCAGCCCGACGGACTCTGTGCTGCCAGCTTGTGAGCTATCTATATTCATTTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACAGGAGGCTGTAGCCAGGAACCCCTCTCTTCCCTGGT CTGGCTCTGTGAGCGG/GC/JTGGGAACCAACACCTTCAGTCTGGTG
WI-19139b	110	C A ---	---		CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGTTGGCAGACAACACTAG/C/AJATTTACGGGTGTGGGCAC ATGGGTGTGGCACCTGACGTGTGCAGCATGTGGCGGTCTGTGTGAAGCCAGTCTCTCTTTGG GGGCCGCGAGATCTAGCATCTCTGAAATCCTGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---		CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA CTGGCAGATGCCCTGACAGAGAGTGGTTGGCAGACAACACTAGCATTTTCACGGGTGTGGGCAC ATGGGTGTGGCACCTGACGTGTGCAGCATGTGGCGGTCTGTGTGAAGCCAGTCTCTCTTTGG GGGCCGCGAGATCTAGCATCTCTGAAATCCTGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---		GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAAGCTAAACATGAAGGAAGGGTGCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGTGTC/GJGGCTCATGGCAGAGCATT CAGTGCACCGGTTTAGG
WI-19235	173	A G ---	---		TCAGGAGGTGGAGTTCGTGTCAGCTCTCTGTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTTCACTGCCAGTATTGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCCTAATTGTTTCAACAATGGTGGAA/JGJGCTTCATGTAATATGATCAGGACCCACO TCCAGTCTTCTGAAAGTGTGACAGTGTCCAGCCGTTCTGCAGCACTA
WI-19222	179	C T ---	---		CGTTTCCCTAACTCACCAGTTTAGTTTGGGATGATTTGATTTCTGTGTGTGATCCCATTTCTAA CTTGGAATTGTGAGCCTCTATGTTTCTGTAGGTGAGTGTGGGTTTTTCCGCCACCAGGAAGT GGCAGCATCCCTCTCTCCCTAAAGGGACTCTGCGGAAC/C/JTJTTTCACACCTCTTTTCTCAGGGAC GGGCGAGGTGTGTGTGTACACTGACGTGTGTCAGAAAGCAGCATT
WI-19117	134	A G ---	---		AAATAATGCAACGCAGGAGGAGAAAGAAATGCACCTAGACAAGACATTTCTCTCATAGAACATTG ATCTGTTTTACAGGAACAACCTTGCCCTTGAAATTTACACAGTGAGACTGTACATAATTCATGAA A/GJTAGCTATTTTTCCTAAGACATTTTTCATTCATGAATATTTTCAAGTTTTCTACTGTACA CATTTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTTG

WI-19134c	263 C T ---	---	CTCCTGTTGTAACCTGACAGGGTGACACAGCCCTTTTCACACTCTGTCTCTCTATCTTCTCTGCGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCATCCCGACAGGGGGTGACGCCAGGGTGCTAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACCTATCTTTTCAGAGCAC TTATCCACTTGTCTCTCTACCTCTACCTCGGCACCTCGGGTGGGAAAGGG
WI-19134a	162 T C ---	---	CTCCTGTTGTAACCTGACAGGGTGACACAGCCCTTTTCACACTCTGTCTCTCTATCTTCTCTGCGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCATCCCGACAGGGGGTGACGCCAGGGTGCTAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACCTATCTTTTCAGAG CACTTCATCCACTTGTCTCTCTACCTCTACCTCGGCACCTCGGGTGGGAA
WI-19224	112 C T ---	---	GGTTTCACAGTCTTCCAGGGAACTCCGATGAAGTGTCCAAACAAATGAGCGAGTGAAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAACAGAGGAGATAATCTCTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTTCATAATCCAGAGGCCAGAAAGACTTCC AGGGAACACTCATTCAGGAGGTGAAAAATGATGGATGACTCTCTCCAAAGATGAAAA
WI-19201	179 T C ---	---	GCAGCTCTAAGGACCACCTGGCCATTAGCTCTGCTTTTGATGGCATCTCTTCCACCTTGTCTTCTC CTTTGCTCCTCTGTGTAGTGTGGCAGGTATGACAACATCATCCAGTGGAAACACAGCCTCACACTGOC CTTCGGCCCCCACACTTTGCCCTGCAGGTGCACCGAAAGGACTCTCTGGGGGATAAAATTCAAAAAA GTGTGATGTGCTGCTCAGAAAGTCAAGACTCATGTCTGCTCTGGCCTCAA
WI-19034	45 T C ---	---	GAAATGGTCCACTCAGAGCTACCCGGTGATGAGGATAGGGGAATCTACTTCTATTACATTAAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGCTGTTTGAAGTGCAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTTCAGCATTTAAGTCTGTGCGAATTGAC ATTTGCTACTTATAAAGTGTGCTTGTGCTTCTTATGCTGCTATATA
WI-19102	25 C G ---	---	TGTTCTGAGTCACGCTGAGGAGAGCTGCTTCACTCAGGAGTTCATGCTGAGATGATCATGAGTTCA TGCGACGTATATTTCTTTGGAAACAGAAATGAAGCAGAGGAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGTCTAGAAGTCTGTAAGTTTGAAGTCTGAGGAGAGGAT AGTGGATGAGTGTGAGCATCGGGCTTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65 A G ---	---	AAAGGAGGAGAAATCTTTTACATAAATGCCTTGATCATCTCTCCAGTCCCTCACTGGGGGAAT G/AAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62 G A ---	---	AAAGGAGGAGAAATCTTTTACATAAATGCCTTGATCATCTCTCCAGTCCCTCACTGGGGG[G/A]A AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97 T C ---	---	GGCAGCAGCTTTTAAATTGAACACTTTCTCTTGAGGACACACCTTCAGTACAGTTAACAATGGT TACACCTGAATCTGCTGAGAGCAGAGCTT/C/AGATCCACAATTGCAAGGCCCACTGCTGGCTCA CTTCTCACA
WI-18501	121 C T ---	---	CAGAGGGAAAAAGTTATTGAGTCAGCCACAGAGGAAACAGAGAAACAGACACAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGGCGGNACAGCTGAACCTGCGCAGGACAGAGGGGCG[C/T]GGACAGCA GCGCATGCCACAAACATTCA

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WI-18017	87 C A ---			ACAAAGAAATGGAAATAGGTTGGGAAAGTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA/C/AJACTGCTGGATAAATCGTTTCAATTAATAATATATCTCTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101 A G ---			TTATTGCGTTCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAAAACGAAAGCA GTGATTCAGAAACCNCTGATTCTGAATATCCGAGTTGGCGGCATATGCAAGGAAGATGA
WI-18254	64 T C ---			TATACGGATCATGTATTTGTGTGACCACCACTACACAGTCAATTTGTAGAGCAGTTAAATCACT/C JGCCAAATTCCTCTGCTTCTGTTAGTCACTCTTCCCAACCCAGGNACTTGGCAACCTGTTT TCGTTCTAGACATTT
WI-18265b	117 C A ---			CAAATGGGTGGACTGAGTGATAAAACGCATATTGAGAAACAAGACGGCCTTCTGGCCNCTGCGTCC AAGCTGTAAAGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG/C/AJGTTTTCAACCTTTC CTTGGTGGTTCTTTCAG
WI-18295	40 C T ---			ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG/C/JTTGGGAAGTAAAGTTGATTACT TCCTCTCAAGGATGATGTTAATGAATTCCTTTNCCTTAGCTTCAATTCATATGCCCCAA
WI-18459b	64 T C ---			GGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTGACACGGGTGGGAGACACAAAT/ CJGAGTAATTAACAACATAATATTTANATGACAGTGAATTAATAACGTCTGGTAAGCCAGAG GGGAGGAGGGCGTCTTCA
WI-22585	56 A G ---			TTATTTTAAATTTGCATCCTGAGATAATAAAATTTATCTGACAAGTGAACAAATG/AJGACAGAAGC AGCAGTGAAGTTTCGGAGAGCAGGTATCCTTCAATTTGGCACAGCTGTATATAGATTGA
WI-21155	36 A G ---			GGCTGTGGAGTAACAGAACTTGATGGAAATTTGGC/JGTTCTGTGTAGAATGATCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88 G A ---			GCCTTTGCTCTTTGCTGCTCAGAGGCCTCAGATGGATACGACGCAACTTCTTTGAACCTTTTAT TTTCTGGCAGGAAGAAG/AJGGATCCAGCAGTGAGATCAGGCAGCTTCTGTGTGCACAGACAG GGAAACAGGC
WI-19888a	98 C T ---			GGCAGGATTCACCCATAACAGAGAAATACTCCTTATTGGAACAAGGTTTTATTTGATATGATG AAAATATTTTGGAACTAGAAAGTAGCAGTGA/C/JTGGACAACGTTGTAAAGATATTAATGCCACT GAACTGTTCAATTTAAATGGTAATTTTCATGTTATGTGATTTACCTCAATTAAGAATGGAACATGT CTTATAATTGTAATACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82 C T ---			TGAGACCATCCTCTCAACAAGAATCAGTCAGTTCAGCACCTAATTTTCCACACTGAAGTCTACG CAATTTTCATGCAGA/C/JTGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTTGTAAT CATATCATCCGTTTCCAAA
WI-20801a	125 T C ---			TCAGAATTGCTTCCACTGCCCCAAACCAAGAAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTCTCTGGAGGTTGCATGACAGGATTAGTCTTCTGTGTT/CJCTTGGT GCAAGTTGAACCAAGTATTAGTACCATTCAGAGGATCTGTTTCCCTGTGATGCCACTAG

WI-20561b	94 T C ---	---	CGTTGCTTATTAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATTG TACTTCAGATGAAAAATCCTTACATGTC/GJGGAATCAATGTCCTTTTAAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20561a	25 A G ---	---	CGTTGCTTATTAAGATGGCTGTTT/GJTAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATT TTGTAATTCAGATGAAAAATCCTTACATGTTGGAATCAATGTCCTTTTAAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20116e	69 T A ---	---	GCTTTCATTTCTGTACCCACCCCTGTCCACAGTTATGTTGGCCTTCAATATATGCGTTAGAACAT AT/ATAAATCTATATCATATATTTATACACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTGGGGCTCTCCCATGCCATTAATAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116c	59 T A ---	---	GCTTTCATTTCTGTACCCACCCCTGTCCACAGTTATGTTGGCCTTCAATATATGCGTT/ATAGAA CATATATAATCTATATCATATATTTATACACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTGGGGCTCTCCCATGCCATTAATAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116a	22 C G ---	---	GCTTTCATTTCTGTACCCACCCCTGTCCACAGTTATGTTGGCCTTCAATATATGCGTTAGAA CATATATAATCTATATCATATATTTATACACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTGGGGCTCTCCCATGCCATTAATAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20466b	133 G A ---	---	AAAGATTTGCAGTCTGGACACAGTTTGGAAACACTATTTATAAGTTGCACATATTACAAACAG NTCCCAAATGGTGAAACTGGTATTCTAAGATGAAGCTTAATGAACATAATGAAGTGAATAAACGGC G/ATGTGAACATAATGTTTAAAAAGTTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTATCCCTTTTATCCCTTTTCCAGGTTCCGATT CTGGGAGCAAGTAACCATTTTAAAGAAATCTCTCAAC/G/AGTTCTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAATCTTATTTGGAACATAATCTTTGTATTTATTCGAGGAAGAATACT ATAAGATTGACTTACTCATTTGTTGACTGGTTTGTGAGCCTTACTGGGG
WI-21034b	148 T C ---	---	AGAATGGACAATGATGCAGATGATTTGTGAGCATTTTGATGAGAAAGTGGTATTAGAAGGATACAG CATAAATTTAATTGTAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAAATTAAGTGGTATGG GAGATTGGATAGAT/CJGCCTAACCTATCTCAATTTTAAGTAATGTGAGCAA
WI-22091c	205 G A ---	---	GGCGTGATTTGATGCAATGTCCAACCAAGTCAAGCTATCATTTGAAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGCAATGTAACATACAGCATATTACCTCCCCCTTAAGTGACTCATAATTTTC ATTACTGTGTGTAGCTTTTAAAGGTTTAAAGTTTAAATGTGTAGCATTAAAGTGGTATTACTTGAGGGCA ACA/G/AAATACGGCTTAACACACACACTAAATCATGAGGCTCAGGGATTG

WI-21805a	45 A T ---	---	CAACTGCTGAGGTCTTCACTAGCTGATTATAATCCTATATTATJAAAAAAAAATCTATAGTCTG CAGTCTTTTGACATACCTCTCAAGGGTGATATGTGTGGAATGCAGATCCCATCAATATGTGTGTT TTGTTGCTTTTGTAGCTTAACCTGCTTTAGNAATCCAGAGGAATATGATTGAGCCAGAGTTA CATTGGTTTCATAAAATTCGAACAGTTGAAGGCTGTTTTGTAAATTGCTG
WI-21778b	155 T C ---	---	AAAAATCCATAATTATTGAACCCAAAGTTACAGAGAAAGTTCTGAATTTTTTATTGAATTATTGAG TCTGCCCGGTGCTGCTGCTGCTTTCAACTCCAGTCTGCAATGCCCTGTGTAGTGGGGTCCCCAG GTCGGGCTTCTGAGGTCTTCGGTAGAAGGAGGCGAGTGGT
WI-20907	241 A C ---	---	TGAGTCAGTGGTCAGATGGGCGAGTTGCGCTCAGCTCAGTCCCTGACTCCGGAAACACTGTGCTCT CAATGATCTAGAGCTCATCTTGGCGTACATGAGGGCAGTTGTTCTAGTACCCATTAGCCG ATGGCTCTCAAGCCAAATTCAGACTGGGAAACACACCCCTCAAGATGCTTATCCATTGAGTTC ATACAGGTTTTAGTAGCTAGAACTAAAAACATTTTTTAA/CJAATTATCTA
WI-21449b	222 C T ---	---	AACAGCAGCAGTCACCTCCAAAATGCAAAAAAATTAGCAATTTTAGAATAAAATTATAATGTTTA TAATGCGGGTCAGAGANTTGAAGGTACAACAGAAATCAATCACGCAGCACTGGAGCGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAAAGTCACAAGAAATCCCAACCTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCA/CJTTCAGAGAGCCAGTGTCTCTGGGTTAG
WI-21558a	157 G A ---	---	GCCTTACAAGGAAGCTGTGGACAGGCGAGNTGGTGGAAACGACTCCAGCTGGAAACCTGCCCTC CCATCCCTTACGCTCTTGGCTTCCGGCTGATTTCTTCGACAGCAGTCTGCGCAGGGCAAGG AGCTGTGGTGGGGGCGAGTATG/AAGCCAGGAGTCCCTCCACAGATGAGGCTAGGGCTGCAA AAGGGCCCGGTGAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178 G A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCGGTAGCAGAGCTCATGGNGACCA GTCCTGGGCTGAACCAATGGGTGATTACATTTAAACCAACCAACAAACAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG(G/A)AAATTTTCATGAAAATTTCC CCTAAACCATAACAAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-22187a	110 C A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCGGTAGCAGAGCTCATGGNGACCA GTCCTGGGCTGAACCAATGGGTGATTACATTTAAACCAACCAACAAACAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGGAATTTTCATGAAAATTTCC CCTAAACCATAACAAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-21609b	146 G A ---	---	TCATGAATATGACGCTCCATAATCTCTCCCTTGTAAACACGTGCAGTCCGTTCCAAAGCTGTAAA AACAAAGCCCAACCCAAAGACATCAAGAGGCAAGAGCAGTGGCAGTGAGAGGAGCCTGTAAAG GATGTTTCAAG(G/A)AGGGTCCCGCTATGTGGCCACTGGATGTAGGCAGTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAA/CJTJGTGCAGTCCGTTTCAACAGCTGT AAAAACAAGCCCAACCCAAAGACATCAACAAGGACAGCAGTGCGCAGTGAGAAGGGAGCCTGT AAGGATGTTTCAAAGGAGGGTCCGGCTATGTGCCACTGTGATGAGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGCGAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---	---	ACATTCCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCCTCCCTAGGGCTTCA GGGTAAAGCCCTGACATCATGTCTTTTGTGATCTGTGACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTTAAGGGCAGGAGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGACAAATTTCTGTCCCTTTTAAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTGTGATGATTGAGCAATCTAGGGG/CJTATGTGACAG TTTC/AJGTGCACTGGTACAGAACAACAACAGGGAGTTTTCACAAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGACAAATTTCTGTCCCTTTTAAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTGTGATGATTGAGCAATCTAGGGG/CJTATGTGACAG GGGTTTCATGCACTGTGTACAGAACAACAACAGGGAGTTTTCACAAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	ACAACATGCCTGTTACAGGGGGGAAATCCTAGGNAATAACTTATGTGTACTTCTTG/AJTTTCA TCATACAAGACAAAGCACAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATTGCACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	ACAACATGCCTGTTACAGGGGGGAAATCCTAGG/AJATAACTTATGTGTACTTCTTGATTTCA TCATACAAGACAAAGCACAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATTGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	AGCCAACTCAAGGCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA/GJAGACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAATACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAGGAAC AGATGTTAACAAAAACAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	CTCTGAACATAAGGGCCGTGAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCA/TJACAT TGCTGGAATGAGGTGTCAGGAAAATAAANTGCACAAATCTAACACCATTGTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGCCCTTAGGT
WI- 22130b	165 C T ---	---	TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGCGGCTGCCCTCTCCCTCTCTGACAC CAGCAAGGGGGAGGCCACCATCACCGGCCCTGCCCATCATGCATCCAAATGATTACTAGCAGCTAGGAA GCCAACGGAANAGGACCCCGCGCTTGCT/CJTGTGTTTTAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGCTCATGCAGTCCCTGTGTGATGGGAATGAC

WI-21661	117 G C ---				GCTTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAATAAACATTATACACATATAAGATCAGTCTTTCCAACTTTAGAAATAGATAAATAAGATGACATTTTAAATAAAAATA[G/C]TTTAGTCACAGTCAACAAAACTACCTTCTAAGGAAAACTGTCCAGTGAAGCCGTTAAATTTGTGCTTTTCAGCTATGAAGGA
WI-21980a	25 T C ---				TCAGTTTAAACACACATTCAATCAAGGATTCJAGATTAATTAATGTCAAGGTGAGCATAAAGGGAGATTATAAACAGAAATGTGTTTTCTGGGAACCAAGTTTCAAGTGAAGTCAAGGATAAGTTTTTATTAAATTTTCATGGGTGAAGCCCTGGGATAAAG
WI-21636	71 A G ---				TGCTTGATTAAATGTGGTGTACATTATCCTATTTCACAGATGGAACAGAAAAATACCAGCTTTTTTAAAG/GTJAGCAATATCTATTATAATAATAATTGAATAACACCAATAATAATATCACTAAGGAAGTAATCTAATTGTGTGATTTTGCAGAGGGAGAAAAACATTACCTTAGAGCTGAGGCTATTGTGCTCATGCAAACTCCAATCTGAAGGTGTAGAACTAGGAAGGGACAGGGATTTC
WI-22457a	112 G A ---				TTGCTATAATTTCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAACTCACTATTAGACAAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACAG/GA/CAGTTAATTAACATAAAGGAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAAATACCTGGGGCCAAACCCACTGAACCTACCCAGCTGAAACACTGAAGGATACTGGGTAAGGA
WI-21524b	97 C T ---				GCCGTGAGGGTTAGCGTATAATGAAGGGTGTAAATAGCCTGATGTACGACCTTCGCGTCATCTTATAATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTCGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCTCCAGGGGATG
WI-21524a	35 A C ---				GCCGTGAGGGTTAGCGTATAATGAAGGGTGTAAATJAGCCTGATGTACGACCTTCGCGTCATACTTATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCTCCAGGGGATG
WI-22652a	32 G T ---				TTACCTTCCAAACCAGGCCACTTTGGAGAAAG/GTJAGAGAAATGCTATTAAATCAATAAGCCAAAGACAATAGGGACTACCTGGGGTAGAACCAGATGGGCAGTCAACCATACCATCATCTCTGCCACAGAACCCTTGACATGCTGCCCTCCCTACTCCGCACTCACTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTTTCTTAGGG
WI-21703d	197 A G ---				CAACAGGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGTGTGTGCTGGGGCAGGGCTCTGCATCCCTTTCTCAGCAGAGCACCCTCTTCAACCCTCTCTGGGAAAGCAGCATTTGGAGCCTACACCACTTGCTGCTTTTCTCACCAGGGTAAGAAATGCAAGTATTTGCAGAGGGGAGTGAGTCTGGGAAG/GJGTGGGCAGAGCAGACTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG

WI-21703c	134 A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGTCTGGGCAGGGCTCTG TGCAATCCCTTTCTCAGCAGCAGCAACCATCTTCAACCTCCTGCGAAAGCAGCATTTGGAGCCTACACQ AGCTTGTGCTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGAGTGAGTCTGGGAAAG TGGCAGAGCAGCAGCTAGGGCAAGGACTTAAGGGAACCTGTGGGGGAAGAG
WI-22663c	139 G A ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCAGTGCAGTGGGAGTGAGCGGCGCTCGCTAATCTTATTC CCAGTCTGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACTTACAG GC/GA/GAAGAGCTTCCTCATTTGCTGAGGGCTTTTCTGAATCCGTGTGAATGTGGGT
WI-22663b	55 C T ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCAGTGCAGTGGGAGTGAGCGGCGCTCTGCTAATCTTA TTCCAGTCTGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACTTAC AGCGGGAAGAGCTTCCTCATTTGCTGAGGGCTTTTCTGAATCCGTGTGAATGTGGGT
WI-22663a	38 C T ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCAGTGCAGTGGGAGTGAGCGGCGCTCGCTAATCTTA TTCCAGTCTGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACTTAC AGCGGGAAGAGCTTCCTCATTTGCTGAGGGCTTTTCTGAATCCGTGTGAATGTGGGT
WI-22668	99 A G ---	---	TCCTTTATCCTGCTGCCTGAGTATTTGGGAATCTACAAGGATTTAGGGAGCCCTTGGGATT CCAACTTAACAAATAGTTTCTGTAATATTA/GTCTAGTCCATTTAGATTGTGTAATGATCTAA ATGNGTAACCAATTAATCAAAAGTATAACAGCATTAAAGTCAGCTTTTGAAGAAACTTTTATT
WI-22631a	52 T C ---	---	AAGATATAGTGGCAGGACAAGATTGGTCAAGAAATCTGGCTCAGTCTGATTC/JAGCACCATTTT CAAGTTTAGGCAAGTATTAACCTCTCAGGCTCATTTCTCTTTGTAAATGTGATAATGGACC TATGTACCATCATAGGGTACTTTGGACAATCAAGTGAAATTTTT
WI-20258	157 G T ---	---	AATCCACACTTTCAAGGAGGGGACCAGCCTGCCATGTCTCCAGGCTCACAGCAGCGGGGCTAC TCTGCTGGTGGTTGGTGGCAGGTGAGATGGTGAAGGCGCATTTGGAACCCGTAAAGGCATGACAACG GGAGGCGCGGGGTGTTTCAAG/JGCGGTTGACGAGGTGCATGGCTGGCAGGCGGCTCTACAGA AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAGTAOC
WI-22714	212 C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAATAACATTTACATTTGTAGAGAAAATCTAGGGTCT ACTAAATAATCTAGTACTTGTTCCTCTCTGCTAATCTGACAGGAGTGTGTGGGAAACGAAAGT CTGAAAGGATTCAGGGGGCTAGGATTTGCAACAGATCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA/CATGAGTAGGGGGCAACATCTTTAACAAGCTAGTTGCT
WI-22734b	44 G A ---	---	TGGGGCTACTTTAGATGGGATGGCGTCAGGGTCTGGGAAGGCTG/JATCTTAGAAGACATTACCCA AATGATGAGAGGAGCCAGTCGTGAAGCCATAGTTGGATGGCAGACTTTTCCGGCAGAGGAAAT AGCAAGTGAAGGGCTGAGGGAGAAATGAAGTGGGCTTGTCTACAGGGTGAAGGGCGCGGT NTGGCTGAGGTTTAGTGATG

WI-22724	117 A G ---			<p>TGATATGATGTCTGAGATTGCTTCCTCCAAATATGCCTAGGAAGGAAGAGTGTAGAGATATAGGA CAAATCAAGATTGTCAAAATGTATAGTAACTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTTGGGAATT</p>
WI-22750	48 G A ---			<p>TGTAACCTGTGTTTCTCTGAAAGTTGAGGGAAGCTGAGGCGAGCTAAT[G/A]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACTAAGGAGAGTCAGCATCTGACCATCTGACTGTGCT</p>
WI-22775a	60 A G ---			<p>TGCTGTTCTTATGTTTCATGACGTTTATCACAATGTGCTACTGTTTCCATTGTTACATC[A/G]T/AGTA GGAAAGGGGAAAATAAACTCCCTAAGGGCAGCAATAATTCTGTCTTTGAATCCTTCATTGAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAAGTGTAGGTATGTAGGTGTTGGGAGCCAGGAAGGAAG GGT</p>
WI-22808	143 C T ---			<p>CTTAGCTAATGAAGTGGCTATGTGACTATGATAGACCAAGAAAGCTACCCAGTCTCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTAAAGCAACCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAAGAGTAGGTATAAGAACCCAGGAGAGTGGGGTCCAAAT ATC</p>
WI-21016	207 G A ---			<p>TCCTCGTGTCTTGAGCCCTCATCCACCCCTCCAAAGCCCTCATGCCACCACACCCGTGTCACATTT CCCCATCCTCCCTGTCTCTCCCATCTCAAGTCCAAATCCAAAGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAGAGGGGAGTGAGATGGCAGAGATGGGGTGGAGCCAGTGGCTGTGGGTG CTG[A/T]TGGCGTGTGATGTGGGGGCCAATCCTGAGGCCAGAGTTCA</p>
WI-21031	31 C T ---			<p>TTGAACACCTGACCTGACCTGTACATGTGG[C/T]CTCTGTGTCCTCCATTTGTCTCCAAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAAACACACACA</p>
WI-21314	122 A T ---			<p>CCATATCCAGTCTCTTTGAAGCTTCTATTGACTTTTAGGGTTCAAGTTATTATATCCTTTATCACTAT GACTTTTCATTTGATTTTATTTGTTTCTCCATTTCTGTCTGTCAAACTTTTC[A/T]TTTGTATAA ACTGTTTCTAACTTCACTTAATCTCTATCTGTATTNCTTGTAGTTCCCTGAACCTTCTTTAGAGG</p>
WI-21186	95 G A ---			<p>AGCGAGCATCAGAATCACCTAGAGGGTTGACTAAAACAGACTTCTGGACCCCAACCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCCCTAAGTGTTCAG ATGCTGCTTGTCCCGGGGAACACACTTTGAGAACTATTGTCTTAAATGTCTCTCTCTTTCTTTAAA GGAGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATAATGTAATTGAAT</p>
WI-21187a	94 A G ---			<p>CCACGATAACTATAAAAGCAGAAAATTAGCTTTGAAAATCAAAATACATAATTTAGTAACACACATT CATTTTATAACACACATAAAGACAC[C/A/G]GNTCTCAGTAATGCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCATTTGCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAACTCTGAGGGTGAGACCAAGCAACCTGT</p>

WI-21190	39 T C ---	---	TTTCCCACATACCAATGCACCTGTTTGTATAACTATT/CJGTGGGGTAAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATTAATTATAACAAATAATTAATTAATCTGTACTATTACTGC TTAGTTATCTAGTGTATTGAGAAAGGAGAGTCAGCATAGTTATTTTCCATGTAATAAAGCTT AACACA
WI-19937d	186 G A ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGAAGGAAA GAACTATTGCACAACCAACATTTGACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATGGTGTCTCCTCAGCAAGTC/GA/JTCCAAACCTTC CAAAAGAAAGCAGTCATTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185 C T ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGAAGGAAA GAACTATTGCACAACCAACATTTGACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATGGTGTCTCCTCAGCAAGTC/GA/JTCCAAACCTTC CAAAAGAAAGCAGTCATTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-2117b	227 C T ---	---	GAAACGGGGTGCTAAACAAAGAAAAGTCTCAGATCCCACTGAAAATCTGTTCAGTTTCACAGGCTC TCTCAGAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAATACATCTCTGGGG TCCAATCACATACCTCAGGTTACAGCTCCTAGCTCCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT OCTCTCATTTCTACAGTCTGATTT/CJTTTCTACTGAATCTTGGGTGGGAG
WI-21122a	42 C T ---	---	TCACTTTGTATCATATCCCTGTAAAGCTAAAGTTATTCA/CJTTAACAGGAACTCTGTTTTC TTATCAAAATGTCACAAGCCTGACGCTTACTGTACATATTGCTAGCAGGAGACAACTGGAATACT AAACAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTGTTGGGTTGCT
WI-21254	53 A G ---	---	CAGTTTGTGTACAGGAAGGGCCCATGATGTGGGGGGAACCTATTCACAGGAG/CJGCAAGGAGAAAG CTGTTCTCTGG
WI-21054	23 G T ---	---	AAGGAACTGCATGGGTACAAAT/GJTCCAAATTCATACTTAACAAGGTGGGGAACGGGTCACTCT TGGCCTGCTCCAGAACAGGGGCGAGTCTATGCACCTCTG
WI-21059b	181 T C ---	---	GGGACCAGGGTAACACATTAGCAATATCGTTATCAGCCTTATCTTCCCAGTGGCTGGCTGAA CTACAGCTGCCAGCATTCCTGGGCTTGCATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTCACTGAAGTCATTTCTCTATTC/CJATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63 C T ---	---	GGGACCAGGGTAACACATTAGCAATATCCGTTATCAGCCTTATCTTCCCAGTGGCTGG[C/JT] GAACTACAGCTGCCAGCATTCCTGGGCTTGCATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAATCCTGGGGAAGAGACATACTCACTGAAGTCATTTCTCTATTCATTTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT

WI-21627b	153 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAAG/GTCCAAAGTCATCTAATAATTAAACCATATTTTACATAAATTTGTAGG GACAGTATAGTAATAGTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21627a	106 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCAGTTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAATCCAAAGTCATCTAATAATTAAACCATATTTTACATAAATTTGTAGG GACAGTATAGTAATAGTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21398a	75 C T ---	---	GGATTGAGTCCCACTGATCTCAAAATTCACCTTCTGCATGTAACAAGCTCATTCCTCTAAAGTT TCAGTTTCTTTCACCAGTAAGGAAAGGTTGGACGACATGTTGGACCGTAATTCCTTGGTAA CTGCTTCTGCAATTTGCTCTGAGGTTGTGTGTCCTAGGACTAGGTAGGATCTCTTGTCTTCTGOC TTACCTAGGCATAGTGCTGATAGCAGGCTGAAGCCCAATTCATCTGT
WI-20323a	68 G A ---	---	CGATGCTGCTAAGATAGGAGTTAATCTTTACATGGTGAGTGCGTCACAGACAGACATCAAT C/GATCTGTTAGCAGCGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTCTGGCTTCTTAAAAACAGTAACCAATCAAAAAGAAAGATTTAGAGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGAAAGCCCTCACT
WI-21249	155 T C ---	---	TTCTGGCATCAAAATGTACATGTAAATCCAAATTTAACAGATCAAAATTTGTACACTAAGTTTCACT TAGTATCTAAGTATCCAAATCACAATTTGATCTAAGTTTACCTTTTAAAGAACATTATAAAGGTAAT AAACTCTAGGTGTATCTTAT/CJATGGAACACTAGTTTATTTCCNATTTAACTACTGTTTCAATTCGGTA AAGTATGTTGCCCAATTTTCAGCTGTTTAAAGGAATTTATAAAACATTGAGA
WI-21504	147 C T ---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAAGGCCATTAGAAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAATTCAGTGGGGGCAAGGCGCTTGGCTCCAGCTGGGTTTCCC AGATGCAACAAT[C/T]GCGGTTCTGGCTTCTCCACTGTGGGGATGGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	CTGCACCGAGGAGACAGCTGCGCAGGAGTAAACCCCTTCCACCTGGCCATGTTGGTGGTGT CTCTATGGACCGAGGCCCTGAACGCGGGCAGGAGGGGCAGAGAAC[G/A]CACTAGCTTGGGGGTG GGCACACAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGAGCTTGGCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTGGTGGCTCCAAACCCAGGCTTCTCACTTCTTACTAAGCACAG CAGTCTGAAGCTTGGACCTGGGCAAGTGGCTCTTTGGAGAAAGGCA/GJAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCGTTCTCCACCCCTATTCTCCCTCCCTGAAG

WI-21475b	117 A T ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGAGGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTGATCTTCTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGGAGTGCGTCTTTGGAGAAGGCAAAAAGCCACAGCAAGCAAC ACTTAGGAGCAAGACCTTCCGTTCTCCACCTATTCTCCCTGAAG
WI-20893d	207 A G ---	---	TGTTTGTTCCAGCCACATCTTCTCAAAGGAACCCACCCAGCCGCTGTGCAGGG CTGTCTTCGGCGTTAAAGTGTACTGAGGAATACAATCATTTGTCACGTAAGTTATCATCCGCACTCC AGGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTCTCTCTCTTTTACAATGCAGT TTCJA/GJACATAACATTGGTAGAGTAAACAACAAACCAAGCCTAAATG
WI-20893c	179 T C ---	---	TGTTTGTTCCAGCCACATCTTCTCAAAGGAACCCACCCAGCCGCTGTGCAGGG CTGTCTTCGGCGTTAAAGTGTACTGAGGAATACAATCATTTGTCACGTAAGTTATCATCCGCACTCC AGGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTCTCTCTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAAACAACAAACCAAGCCTAAATG
WI-19941c	71 C G ---	---	GAGCTCAAGGGAAGACCTTACCAGATAGGACTAACTGGAGGGGTGAAGAAACAAGGTGAAA GGTATC/GJGGTCTGTGTGAGACAAAGCAGGGGGCTGAGAACACAGAGAGGTTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGGACATTTCTTATCCAGTGCATGCCCTTAAAT AACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAAAGCAAGCG
WI-21552b	166 C A ---	---	TGGGTACATGGACAGATGTATATGTTATGGGTTATATGAGATATTTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGGATCTCTTCACTCAAGCATTATCCATAGTGTACAAAGAA TCCAAGTATACCTTGATTATTTAAAAATGTA/CJAATTAATTTATTGAATTTAGTTACCCCA ATTGTCTATCAAAATATCAATCTTATTCATTCTTTGTAACTATTATTGTGA
WI-21552a	66 G A ---	---	TGGGTACATGGACAGATGTATATGTTATGGGTTATATGAGATATTTTGATACAGATACACAATGTG /ATAATAATTACTTCAGAGTAAATGGATCTCTTCACTCAAGCATTATCCATAGTGTACAAAG AATCCAAGTATACCTTGATTATTTAAAAATGTAATTAATTTATTGAATTTAGTTACCCCA TTGTGCTATCAAAATATCAATCTTATTCATTCTTTGTAACTATTATTGTGA
WI-21512	54 C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCAGAACCTTACAAAATATTCTGTCTGJTAGAGAGGGA AAGAGCTGGTGGCTGCTCTGGAGGCAACGTCCAGTCCGGGAAAGGCACTGCTGTGATCTGTC TCAGTATGGGAGGTCTCCACTCCCTCCACAGGAGCCTCGGGCCAGAGATGAGATATGCTGTAA TCCAGTACAGGGGCTGGTGGTGGGTCCTCCCAACAGCTCTCTTTGGGG
WI-21513b	192 G A ---	---	CACATAGTTTCTCAAGAAGAGGATGAACCTGAAACTCCTCTAAGGAGGACAAAGCAACTTCCATT ATTCTTAGTTTAGACCAGATCTTTAATTTTATATTCTCTTTAATACTGTCAAAATACACCAATA CTTAGAGGAAAATATTACAGATATACCAAAACATTTTAAAGATAAAGAGGCAGTGA/GJAGTAG TATTCTCTACATACCACAGTATACATGATGCTCTCTGAGGTTTAGGAAC

WI- 21514b	133 C T ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTGCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGCJC /TACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGATTGTCAAGGGTGCATAAGGAACT
WI- 21514a	100 A G ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTGCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGATTGTCAAGGGTGCATAAGGAACT
WI-22020	27 C G ---	---	ATGAAACATGTTGCAGTGGGATGAATC/GJTTCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATCTTACCTGTATGAGGGTACTT
WI- 19576a	113 A G ---	---	TTCATCGGTTCTTAATACAGTACAATCCTTTTGTGAACAAAAAGTCACACTGGCAATGATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATTC/GJTCTAGTTCAGTGATTAGT CACAGAANTTAAACATCTGCCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGA G
WI- 21695a	141 A C ---	---	ATACACAGGCCACAATTGCAGGATGGAAAGGAGTGGGCACCTTGAAGTGACTACACATGGCAATA AGCAGCCTATCTTCTTACCAACCAGAAGTTCTTGGGGCATGTGATGGTAGGCCAGACCCCTTTCCAA GGGAATA/NCJTACTACACTAAGCCTACACTGTACTGTGAGAGTCATGGTGAACAAGGCCACAGGC AGTGGAGGAAATGTGATGACTTCACTGTGTTCAGANTTCTAAGGCCAGCAT
WI- 21574a	235 C T ---	---	AAACCCAGAAATTTAGGTACTTTTGTATTATGAGGAACTCACTATCTAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTTCACACTGATCTGGCAGGTGACAGCTCTCAGTGAACAGGCG TCATCACTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGCAGGCCAGGGAACCTTACTGCCTACTTCTCTGTCTGTCAGGTGGGA
WI- 21644c	151 T A ---	---	TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGTCACTTAACCTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTACCATANTATTTAACAGACTCAAGTGATACATAAAGCTTG TTTCATAAATAAGGGA/T/ATTCATCAAGATCCATGGAATGATGCAAGTTTAACATGTGTCTCAGC TTGCCTACTGACCACCTTCTCTTCTAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55 G A ---	---	TGCTTTAACCTCAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTATC/G/A/TTTTAACA AACCTCATATGATCACTGTGCAATTTCACTCACCTAAATACGGAACCATGACTATTATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGTATTCTTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151 C T ---	---	GACCGAGAAAAAAGTCAAGGCATATGATGTTTGTGGAAGTATCAGATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTTACATATTAAGATAAGGATGGACT CTTCACTGAGTATTATCTJAGGACACAATCGACGGATGTATCTATTGANTTATACCATAGGCCCC TATTCTATATTGGGCCAAAGGGAAAGGTAGGTGGTACTGTGGAAACGGA

WI-21981	61 T A ---	---	TGTCATCTCATTTCTGGAGAAATCATAGATGTGGCAGAAATACATAATTTCTTGAAGAAAAAAATTAAGTCTCCCTTATGGGTACTGTGAATTTCAATAGGGTGGGATAAGTACATGACAACATGCAATGGGATAGACACTCTGTCTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAAGGATATAATGATGGGTTATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGTTAAATTTGG
WI-21660	120 C T ---	---	TCCCACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGGTGAACACGCTCTCCACTGCTTACTGTGTACCAAGAGGCAGAAAGCAGCTCACCCAGCCTAACCTGGCCCTCTTGTCTTTTTCAGGCTTCTCAGGATGCCACAGACATACTGGGAACCTGGGATGCAGGGAGAACCCAGGGTCTGTCTCAGGAGGTCACAGC
WI-19105c	211 C T ---	---	TGGAAGTAGGCCCTTCTGGACAGAAAGAATATTTGTGGTCCATGTGGTTTGAGTCTGTTAAGAAGGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCTCCTGTGTAGGTTTCCAGGGCTGGCACAGAGGTAGGGCAGAAATNTGGGGTCCACAGTGGATCTCCCGACAACCTTCCTTCCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-19105a	33 T C ---	---	TGGAAGTAGCCCTTCTGGACAGAAAGAATATTTCTGTGGTCCATGTGGTTTGAGTCTGTTAAGAAAGGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCTCTGTGTGTAGGTTTCCAGGGCTGGCACAGAGGTAGGGCAGAAATNTGGGGTCCACAGTGGATCTGCCACAACCTTCTCCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-21760c	81 C A ---	---	CAAACTAGTCACTCTACTGATGCAAAATGATTTGGAGGTGCTTCTCTAGCTTTACAATAAGNGGAGCCTCTGACTGCAICATCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAAACTAGTCACTCTACTGATGCAAAATGATTTGGAGGTGCTTCTCTAGCTTTACAATAAGNGGAGGGACCTCTGACTGCACTGCACTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	TCTGCCATATTGTTCCAGCACCCTATTACTGTTATTTCTCTTTGAGGAAAAACCAGGNATTAAGAAATCTGGTTTGAATTTCCATGATGCCCTAACTCTATGTTAAAAATCCTTTTCTTACCAAAAAGGAACCTTCTTAATCACCCAGAGAAACAGAGGGAAGACTGAGATATGTTGCAGAAATTTATCTCTACTCTCTAGAGACAATTCATAGTTTCATAATCTTTTCAGGGTGTGCTTACTTGGGGGGC
WI-20834a	72 T G ---	---	CCAACTGCAACATAGTCTTCTTCTTAAAGATACATAGTAAGGTATGAAAAACATTGTGATTTCAGAGAAATGTTCTAAGACAAATGTGTCAAATATTCAAATGGCTGGCACTAGTGGTAATTCAGCAGACAAACAGCATGAGAAAAAGGCCGGGAGACAGTAATAATACGTGCCCATTCGAATGAGTTACCCCAATCAAGCCCTTTTACCTCCTTAAGATGCGCAGATTAGAAGACCTTNTTCCCAAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATTCAGCCGGGCCATCAGAACAAATAGCATCTATACCTTCGAACCTTGJCCCTCTTAACCTCTCCAGGCAAGAGGAAAAAGTGATCATATTGAATTCCTCAGAAATGGTGGGATCTCAAGACTTTTAGAAAGTGCTTATTAAGTATAAGAGGCTTGAAATATAATGATGATAAATGATAGCCTTCTGGAATAAATTTTGTGTAATCTGTTTAAAAAGATTTTTTGGATGCATTGTCCCCA

WI-21981c	200 T G ---	---	AGCTTGGCTTGAAAATTTGGTACTACTACCTTGCAAATCTCTTATTATTATTATTACTTTATTTTTCGGTAAGTTATTTGGGTACAGGAGTATTTGGTTATAAAGTCTTTAGTGGCGATTGTGTGATTGGTGACCCATTACCCAAAGGAGTATACACTGCACCATACTCGGTCTTTTATCCCTCGCCCCG/G/G/C
WI-21981b	73 G A ---	---	TCCCACITTTCCCTCAAGTCCCAAAGTCCATTGTATCATCTTATGCTAGCTTGGTCTTGAAAATTTGGTACTTACTACCTTGCAAATCTCTTATTATTATTACTTTTATTTTTCQ/G/ATAAGTTATTTGGGTACAGGAGTATTTGGTTATAAAGTCTTTAGTGGCGATTGTGTGATTTGGTGACCCATTACCCAAAGGAGTATACACTGCACCATCTGGTCTTTTATCCCTCGCCCCCTC
WI-21981b	73 G A ---	---	TCCCACITTTCCCTCAAGTCCCAAAGTCCATTGTATCATCTTATGCTAGCTTGGTCTTGAAAATTTGGTACTTACTACCTTGCAAATCTCTTATTATTATTACTTTTAAATGAACCTCCACTTGGGTCTCTTCAAGTGAAT/G/TTCTCTTTCGTTCTGTCTTAAAGCCTTTTAAATGAACCTTCCATTCTGTGAAACTTGCCTTAGTCTGTTTTCTGCTTCATGCCCCCTCAGTCTGAATCTCTTCTTCCACTTCCACCGGTAACAGAGGGTTACATTATGGGGTCCAGGTTCTATCTGATATGGCTGCCCTTTATTTAAGAAATGTTTACTGAGAACTGTACTGTAAACAACATATTTTTGTAGAACATGAGTGAGAGTGTGTGTGTGCGCGCGCGGCAAGGCATGGCACTGAGGGATTGCAATGGG/G/A/AACAGGATAAAAAGGTATAAAAACCTTGTGCCGAAATCTTTGCTTATTAAACCTTGGCCCTGCTCTCACAAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21986	148 G A ---	---	TATACTGGTTTTGGTTACATGATGAATTGTCTAATGGTGAAGTCTGAGATTTTAGTGTACCCATCACTGAGTAGTGATGTTAOCACAACTTGAGGCTTTTATCCCTAACCTACCTTCCACCTCCCCATTTTGAGTCT/G/C/CATAGTCCATTATATCACTCTGTATGCCTTTCATACCCATAGCTTAACTCCC
WI-21930c	146 G C ---	---	GCTCTAGTGAAGAAATTCAGGACGGGTCTTCAGAGCAGAGGGCTTGGTCAAGTCCCTGTTCTGCCCACTTAATACTGCATGACCTTGAGCAAGCCACTTAATTTCTGCTCTCTTCTGTGAAATGGGTACAA
WI-21139a	165 T C ---	---	TGTGGGTGACGAGTAAGGAACTAATACATTCGTACAGCACTTCAGCACAAAGCCTGGGCACACAGCACTGCATGGAATACACAGGTAAACATTTTAAACAGTGGGGACAAAATTTAAGTACGTGGCCAGCGTGTGGTGTCTTGTGGTCATTAAAGACAAATGTTAAGANTCAGGAGTACTTAAAGTGTAGTGTGTACA
WI-20317b	217 G T ---	---	AATTTGTTCTCTTCAGTTTTTCATTAAAGTAAATCTAATAGATGATATACATATTACTGCAGATAAAACCATCATCAGAAA/G/TTTATTAAATTAATGCATATTTTGAGGCTACTCTCAGGACTTGGTTGCTGTCCCACTGCACATAAATGTCCCTTTTGTGTGAGTTATGGTTGTGTGCGTTTTTCCTTTTGCATAAGAAATATGTCATTTAGTCCAGAGGCTCTTGCTTTATCCGATGACGGAGGTACACGGGGCGTCCGCTCAGTTCGCCGCGGAGGACGTATTG/A/CTGAACCTGGGACGAGTCTACTCTC
WI-22082a	179 G A ---	---	CTCCCCACAGGAGCCACGATTTCAAATCCTCTTTGCTGCAACCTCT

WI-22082b	67	CT	---			CAGGACTGGTTGCTGTCCCACTGCACATAAATGTCCTTTTGTGTTGAGTTATGGTTGTGTC/C /TGTTCCTTTTGCATAAGAAATATGTCATTAGTCCAGAGGCTCTGCTTTATCCGGATGACGG AGGTACACGGGGCTCCGCTCAGTTCCGCGCAGGAGCTATTCGCTGAAGTGGACGAGTCTACTC CTCCCCACAGGAGGCGACGATTTCAAATCCTCTTGTGCAACCTCT
WI-20993	139	AG	---			AACACAACTCCATGCTTCAAGATCCACACCCAGATACTAAGACATATTAAATTTACAGCAAT TAAACAGTGTAGTTGTACATAACACATATAGCAATGATACAAATTAGGGGAAATAACCCCTGG GCTTCTTAAAGTGAAGTATACATTAAAGACAGTATTGCAGATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTCAGGCTTCTCTAGCTCATCCACACATCACC
WI-21723b	125	AG	---			AAGCGATTTATTAAATGATTGGACATACTGTAGGTCAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAGGGTTAGTCATATCCCA/A/G/CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAATC ATT
WI-21723a	82	GA	---			AAGCGATTTATTAAATGATTGGACATACTGTAGGTCAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTC/G/A/CATATAAATTAGTAGCTTCAAAGGGTTAGTCATATCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAATC ATT
WI-22132	99	TG	---			CAACAGATGCTTGAGCCAAAAGCAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCTTTACTATCCTTT/G/CCCCATTTCTCTAATCTCTTTGCTTACAA TATATTACCTTCTAGGTATCACTCATCTATAGGAATGCTTCTAGTTAATGCTGCCCCCAACA ATACTAACCCATTGAAGGATAACTATGGAAACCTTTAATGGGACAGTGGG
WI-21008a	106	AG	---			TGACAGATCACACCACATTTTGTGTTGTAACCTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAGAACACATACACACATGTGCACACAC/A/G/AGAGGCAAGTACAAAAATGTAAAC CCACAAAGTGCATGTGAATGAAGTGCAAAAGGCTTCAATTTGCAAACTCTGAGGATCATCTCT CTGCTTCAGGAAAATAAACAGAAAGGTCCTAACTGCCCCAGGCT
WI-21761b	138	CG	---			CTGAGGCCCTGCTTAACCTCATNTGACGGAGCAGTTTCTGGCTTGGAAATAACTGAAAAGATTCAAT TTTCTCTTTGTGTACAAAGGATTCAAATAATTTTCACATCTCTCTGCGAGTTAAACGTGCCGTGG CTT/G/CAATACACACCAAGCCAGCGTAACCTTGGCTGCTCAGGAAGGCTGGGAGGAGTGCCAG ATGGTA
WI-21079c	166	GA	---			AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGTCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAATTAAGCTGTGTGCTCACTTGTTTACATAA CTCAGGCCACCTGAAATATCTGCTAGTGGG/G/A/AAATTTACAACCCAGTCACTCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGCAAT

WI-21079a	50 G ---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTG/AJCGCAAAATCAAGT TGTTTTAATACCAGTGTGCAGCTTGATTCCTCCATGAATTAAGCTGTGTGCTCACTTGTTTACA TAACTCAGGCCACCCCTGAAATATCTGTAGTGGGAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45 T G ---	---	TCTGTAGATTTAGCCATGCCATATATTAACTTTTAAAGGAAAAGT/GJTTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCATTAAGTTAGCTTAACAGTTAACATTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTACTACATTTCAAATATAAATAATTTGGTTGCAAAATTCAGNAAAGGGCA TTAACCAACATGGGACTGATCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21841	79 A G ---	---	TGGAGTTAAGTGGGCTCTGCTATTTCCCCAAAGAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGCAGAC/AJGGATGAGGCTCTTCTGTAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGTTGGAGCCTCACCCAGAGAGCCTCACTGCATTGACCCACACCCACCACTCAACC CAGCACAGGCACACGCGGGCACACGCACACAGNTGCACTCAACCACG
WI-18916b	42 C T ---	---	AATGGCATCCCTGTCGATACCAACATCTTCAGCAGCTCAGC/GTGGCTTCCACTTCTTGGTACCC GGTTAACTGCCAGGNGGTGACAGTGAATGCCAGGGCTGCCCCACTACTGCACTGGACACAGCCTCAACC AATGCCACCTTCATA
WI-18916a	35 G C ---	---	AATGGCATCCCTGTCGATACCAACATCTTCAGCA/GCJCTCAGCCGGCTTCCACTTCTTGGTACCC GGTTAACTGCCAGGNGGTGACAGTGAATGCCAGGGCTGCCCCACTACTGCACTGGACACAGCCTCAACC AATGCCACCTTCATA
WI-19828c	200 A G ---	---	TTCCCTTCTCCCAAGAAGTGGGCAGAAAAGCTTTGTTAACTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTCTGTAGCTAGTGCAGGNTCTTGCCCCCAATCTGGGTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTTCTGACCCCTCACCACCACCAAAATJAG JCTTTTAACTCTGAAAAGAAACCCAGCTGCACACTGGGCACACTTGAOCT
WI-21863b	47 C T ---	---	CACAAGAGTCTGTACAACCTTAGGGACACAGCCCTGGCCCTGCCCTC/JAGCTGCATGCCAGCCTC ATATCCACCCCATCCAGCCTCTGCCCCGACACCCAGGCTCCCTGCTCTGTGGTTGAAGTATTTT CTCAAAGGCAGGAATGAGTCTTGATCCAAACCCAGCATCT
WI-19860	51 C G ---	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG/CJGTGCATCAGTAT CTCCATCCACATAAATTTCTGTTTGAATTTGGCAATTCACCCATAAAATGTGGGATCTACCTCCCT CCTTGCAATTTGAGCTGNNCCTCTGATCTCTAAGGATCTGAAGCC
WI-19889b	80 C T ---	---	ACCCAGCTCCTCTTACCCTGCGCTTCAGTAGGCTTTGGCTAATGGCCANTGAACCTGCAGGGCAAG AGGAGTGAGGGG/CJTAGCAGCATTTATTTCCCTCTTTCACCTCCTTGTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCTTGGCCACAGTGTGAATTTGC

WI-22202	128	A G ---	---		TGTTGCTTTGGTTGTTGCTTCTGGAAACATATTGGAACACTTGTGTTTTCATAAGCTGCTGACAGT GGCACAATCCCATCCATCTTCAGGCCCTTTTAAAGGTCATTATGAAATCTGAATTTCTT/GJTAAAT ACTCTGGTGCAATTCATTCATCTGCAAAAGCAACTGGCACACCACTCTTGGCGGTGCAGCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTGCGGAACCTTCTCCAGCTCAG
WI-22189	70	C T ---	---		CCAAGGATGAAATTCACATTTATTTNCTTTATGTGAATAGAAAATGGCAGTGAAGTGTCTCTATG AACTGAGGCGAGGAATGGGCATGGCGCTGCGGTACCGCTGGACGTTGTCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109	T C ---	---		GGGAGGCATCATAGAAAAAACCCCTCAGCCAGAAGTTAGGACATTGTGATTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCTCAGGCTCTGTTGTCATTTGCAAAATAAAACCCA GACCGGTCATCTTCAGTCCCTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACCTCACTCCAAATGATGCAAAAG
WI-22290a	136	C T ---	---		GACGTCATCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTTATGGGCTCTAAGCACCG GCCAGTAGTGGGAATGCCATGCAATGGGTGAGTGGGATCTGGGGGGGTGAGGACCTTGTCTTT TCCTTCCAACTCTCTCTTAGCCAGAACTTTGCGAGAGCCCTTNAATTTCTCTTCCCTCTATTCC CCTCCTTCCCAAAATGTGCTAAGTCCCAATTCAGACCCCTCCAG
WI-22292	53	A G ---	---		CCAGTGAAGGGTTTACAGCCATAGTGAGGTTCCCCATTGCTCAGTACCCAGAA/GJGTTTGAGTAC GGTCGTTTAAAAAATAGTTATCTGACCACAGTGGAAA
WI-22387	186	C T ---	---		ACCTTGACACCTGCCATCCGGTGCCATCTCCTGGTGGCACAATATACCCACTCTGGCTCTGAAG GCTTGTCAACCAAAATGGGAGCTGGGCTAAGGCATATTTAAACAAGGCTCCAAAGGACCCCTT TCACTTGGGTCTAGCATCCAGCTCTCTCAGCAAGGCGAGATTGTGGTCT/CCTTGTGTTTCTG AACAGGGCCAGGGCAGCCAGGCGATGCCATCACTGCGCACTCAACCT
WI-22395b	127	A G ---	---		GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTCTTCTTGAATATTT GTAGGGATGGATGAATTGAAGTGAATTAAAGTCAAGATAAAGGGGCAACTCTTTAAT/GJAAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90	A C ---	---		TTTATGGCTCCTGAGTGCCCTTACCCAGCTACACTTTACCTTGTATCTATATAAAGTGAATTTAGAGT AAATACATTGGCTGTAAGTCGAC/GATCAGTGCTCTCCACCAAAAGCAAACTGCTGA AATGTGGCAAGTTTCTCAGTG
WI-22419b	67	T C ---	---		CCCTCTGGACAGTTTGTCTTATGTGTTGAGACAATCAAGGNTCCGCTTCCAGGCACAGCCAGTGCT /CCTGGATGGCATCAGCAGAGCTCCCTGCCCCGGCTTGAAGCATGGCTGTGTGTCACGAT
WI-21342d	59	T C ---	---		ATTTCCCTTCTGTGTTTCGTATTTCCCTTTTGTGAGTAAATNAGCAATACACTGAT/CJTGGAA ATCTGCATGATTAATAACATTAAAGTTTCATAAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTCAACCGAATGCAAAATTAGGTATCCCTCAAAATTCACATTTCTCTCTAGTT

WI-21763b	154 A G ---	---	CATACCCCTTTAGTGCCACACATTGATCTTAGTTAACAGTCTTGAGTTCCTCTTTAGGCTTCAAGA TAAATTGTGATTTTCATCGCACCCAGATACCTTCCAGTGAGCCAGGCTCAGACTGTTCTCAGTCAGCT GCTCTCCACAGCTGATT[G]GJGAGACATTGCGCTGTGCTTCTTACCCAGCAGCTGCTAGTGACATT GA
WI-21763a	135 T C ---	---	CATACCCCTTTAGTGCCACACATTGATCTTAGTTAACAGTCTTGAGTTCCTCTTTAGGCTTCAAGA TAAATTGTGATTTTCATCGCACCCAGATACCTTCCAGTGAGCCAGGCTCAGACTGTTCTCAGTCAGC TC[GCTCTCCACAGCTGATTACAGACATTGCGTGTCTTCTTACCCAGCAGCTGCTAGTGACATT GA
WI-22440	64 A C ---	---	CAGTCCATTTGAGTCCCCAGTCGAGGGTGCACTTCTTCTTTATCTTGCTTAAAGCCACTTGGGTA[AC] TCCATTCAGCTCTGCACCTTCTCCAGTTTCTCATGTGCAGAAAGTCCCTGGAGGGAGGCTTCTTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGAATACAGTAC TTCCTTTT[C]GAAAAAATACACAATGGGAACCTGACA
WI-21965a	112 A G ---	---	CAGGTTCCACAGAGGCTTTTATTCAGCCACTCAGGACCCCTGGCTTCTGCTCCAAGGCACCTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGACCTCCCCACAGCCAGCCACAGGGTTCTCTGTT TCCAAAGTCTGATGATTACAGCAAGACCTTCACACATTACCCACTACCTGCTGGAGAGGAGGTC ATGAGGCAGCTGTGTGGTCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGTTTCCCTAGTCAGAAAGTCTCATGGACTTCTTCTCCTAAGC[G]GTGTTCTATGATCAGAC CACCTCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAAGGAGCCTGAGAAGAAATTCACAACCTATTGACTATACAGAG TCTTCAATTCACAAAACAGTTAATAGTAACCTTGGTGACATACAACATGCATTGGAATACTCTGTAT TATTCAGTAACTAAAT[C]AGGNTCCTGCATCATCTCTTCACA
WI-22250b	132 C T ---	---	ACTTGCTTCAGGCAGGCATTTCTGGGATCTAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAAATGTGCATTCAGTGTAGTGGTTATTATGGGTCCTCTGCTCCTGCTGTGTTATG[C/T] GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGCTTCAGGCAGGCATTTCTGGGATCTAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAAATGTGCATTCAGTGTAGTGGTTATTATGGGTCCTCTGCTCCTGCTGTGTTATGCTG GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGGCATCTCTCTCCAACACCTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGCCAGCAGCAC CTACGTGGCCCGAGTAOGGACCCGCTGGCCCAAGTTCTGGCTCTCAGGACGTCCACAGCAAGTGA GCCAAGAGTTTGTCTGGACTCCAGCCAGGGGATGAGGCCAGGCCCAACCTG[C/C]AGTGTCTTC TTTGACCGGGCCCGCTGCTCAGCTGCTCTGCTGAGGAGTGAAGAGGAGGT

UTR- 04932-2a	149 C T ---	---	GGAGCCATCTCTCTCCAAACCTTCCAGGCTCCAGGCTCCCTGGGGCCAGAGCACTCATGCCCCAGCAGCAGCTACGTGGCCCGAGTACGGACCCGCTGCCCCAGGTTCTCGCTCTAGGACGTCAGGACGTCAGGAGTGGAGGCCAGAGTTTTC/TTGGGACTCCAGCCAGGGGATGAGGCCAGGCCAGGCCAGAACCTGGAGTCTTC
sfFIBBb	412 G C ---	---	TTTGACGGGGCGCGCTCAGCTCTCTGGGAGGTGAGGAAGGAGGTGTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTCGCGTGAGCAGCTGTGATTGTGCCACGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCGCCCTCTCTCTGATCATGCGCAGGTTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGAAGGACCATGCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
sfFIBBa	341 T C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTCGCGTGAGCAGCTGTGATTGTGCCACGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCGCCCTCTCTCTGATCATGCGCAGGTTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGAAGGACCATGCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
slGLV2	61 T C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTCGCGTGAGCAGCTGTGATTGTGCCACGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCGCCCTCTCTCTGATCATGCGCAGGTTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGAAGGACCATGCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
slSG1001 7c	70 T C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTCGCGTGAGCAGCTGTGATTGTGCCACGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCGCCCTCTCTCTGATCATGCGCAGGTTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGAAGGACCATGCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
slSG1001 7a	33 G A ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTCGCGTGAGCAGCTGTGATTGTGCCACGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCGCCCTCTCTCTGATCATGCGCAGGTTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGAAGGACCATGCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
slSG1002 3	63 A T ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTCGCGTGAGCAGCTGTGATTGTGCCACGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCGCCCTCTCTCTGATCATGCGCAGGTTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGAAGGACCATGCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
slSG1009 6	36 G C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTCGCGTGAGCAGCTGTGATTGTGCCACGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCGCCCTCTCTCTGATCATGCGCAGGTTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGAAGGACCATGCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
slSG1011 8	107 C A ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTCGCGTGAGCAGCTGTGATTGTGCCACGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCGCCCTCTCTCTGATCATGCGCAGGTTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGAAGGACCATGCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
slSG1012 0	89 T C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTCGCGTGAGCAGCTGTGATTGTGCCACGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCGCCCTCTCTCTGATCATGCGCAGGTTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGAAGGACCATGCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
slSG1017 8	42 C T ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTCGCGTGAGCAGCTGTGATTGTGCCACGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCGCCCTCTCTCTGATCATGCGCAGGTTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGAAGGACCATGCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT

stSG1019 3	136 G A ---	---	GGAACAATACTACCTAAGGACAAATACTATTATTAANAAGTCTTCTAGTGATATTGTGTAA CACATTTCTGGAGCTGGTAGGAATAACCAATTTTATTTTGTGTAGTGCCATCTATACAACTTTTAC TIGAJTTTGAAAACGTGAGATTTAAGTTGCAAACT
stSG1020 2c	143 G T ---	---	AAGCTAACCTTAGGTGAATGTGGCCACTCAAAGTCTTTCCGAGGGAAGCTCAGTCTGGCTTGGGAG AGTCAGCCTTGGTCACCTCATACGGGGCTCCAAAGCTAAGCGCTCAAGGAAGCAGTCCCACTGCTTCT CGCTGTCAIG/TCAAGACACAAAGGCAGATGCCACTGCTGCTCTTTCTTGTCTACTTTCT
stSG1020 9b	75 A G ---	---	TCCTTTCTCTTTTCACTCTCAGTCCACCATGATTCAAATAAACATACTCTCTTAAGATCCCACTTTAT TTTTTA/GTCTCCAATAATGTAAATTATCAGCTGCTGAAT
stSG1020 9a	34 C T ---	---	TGCTTTCTCTTTTCACTCTCAGTCCACCATGATTC/AAATAAACTAATTCCTCTTAAGATCCCACT TTATTTTAACTCCATAAATGTAAATTATCAGCTGCTGAAT
stSG1021 8	29 T C ---	---	TACTAGACATGCAAAATGAGAAGATTACAT/TCGTGAATATTTAAAGAAGTTATATTGTTTGACAT AATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTCTGA
stSG1025 2	108 A C ---	---	ATAGGTTTCAGGAACAAATCAATTAAATGGAAATGAGAAGAAATCTTTATTTTGGACCAATTTT AGGCACCTTAAGAGTTTCTTTCTCTCTTTCCCTTTGATCA/AC/AGTGAAGATATGATAGGGAATTC AGAAATTTCTCTCTTG
EST10915 0	123 A C ---	---	CTGTATTAAATTAAGAAGGCACATTAAATGAGGGACGGAAATCTACCTGTACACAAAATCTGTAC TTTAACAGCATCTTCAATAAACCTTTAAAGGATAATGGTTACGATCATTTTAAAG/AC/JATTTTAA GAACGTAGTTATTGGAC
EST11023 1	166 T A ---	---	TTTTTTGTTAAACCAACCCCTGAAAGTTCCACATGTGAATATAGATACAACAGTGAACAAAT ATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCTTATACACCAAGTAAACAGCAGGGC AATTAGTCAATTAANAATAAGTACATGTTAT/AT/AGTGTAAATAAATTTAAATTTACAAAGGCTTT TCCACTCGTGGATTGATTCCTTTTGGAGGGAGTAACTCTGG
EST14098 8	71 G C ---	---	GGGATGTATATTACAGATAACACAACCTCAACAATATACCATCAGACATTGAAAAGTAAAGGCCATTCT GTGA/GC/JTTATTTTAAACTTGGTGTGTCACATAATGATCTTAAAAAATAATGAATTACCAAA ACCAAGATTCTCTTAAATGAAAATTTAATGCAGGTACAGGATAAGCTTTAGGGCTATATCTAATC TGAAG
EST22113 8c	125 C A ---	---	TGCAAAATGTGAGAAGGCAGAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGATGTGAGGTGG CAGGGATGCTTAAGTCTCTCTGTCAGAGACCCGAGGTGCAGAGATGATTTCTTCTCA/C/ACCCCTTC TCTCAGGGTGTGGAG
EST22555 7	60 G A ---	---	TCAAGCATGTGTAAAGGCACGTGCCCGCCAGACCCCTTCTAATCTTGCACACTGGAAGGTG/AJAAA CCTGGGAGAGAGAGACACTCCCTCCCTAGCTTCTACCTGGGCAACCTCCAAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGCTCAGAG

EST22917	74 C T ---	---	---	GTAAACCTTGCAAACGCCATGCTAAATGGAAGCCCTGACTGACCCAGGGGCTCTTGGGCTCTCAATGCA ATAGAAA/C/TTTGACATGGGCCAAAGACTTCCAGACAAAGCACGCGAAGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST38458	65 A G ---	---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCCCTCAGGCTGTCTACTCA/VA GTTGGTTTGTAGCCTCACTGCGACACAGGAAGCTTGAATTTGGAGGCTCCAAGTCACTCTCCA
EST38745	56 A G ---	---	---	GAGGGGGAACCTTCAAAGAGGATTCCAACAGTGAAGCAGAAATCATGGGGCAAAGTCA/G/CTATGG GGCCAGACTGAGGTTGGAACACACAAAGCACTCCAAGCTGGGCAATCCCAACCGCTGGTGAAGCCGC ACAGCAGGAGTAGCCAT
STS- R37410c	201 A T ---	---	---	TGTGACCATACCAAACCTATGCAATAAAGAAAAGAAAAATCCTCCTTAAAAAAACAAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTTCTGGTATG T/ATTTATTTGAGTGGTGTCTAGTGCCAAAT
STS- R37410b	139 G T ---	---	---	TGTGACCATACCAAACCTATGCAATAAAGAAAAGAAAAATCCTCCTTAAAAAAACAAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGAGTGGTGTCTAGTGCCAAAT
STS- R37410a	48 C T ---	---	---	TGTGACCATACCAAACCTATGCAATAAAGAAAAGAAAAATCCTCCTTAAAAAAACAAAAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTT GGAATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGAGTGGTGTCTAGTGCCAAAT
STS- R42778	74 C T ---	---	---	TATCGTGGGAAGTTCCAACCTCATCTTATGCTGCTTTCTACTTGCTAATATTGGATGCTCTTGCCA GGCTC/C/TTTAAATTGTGCTGTAACTGGGAAGAACCTTCTACTCTCCACAAACCTGAA CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGGTTTCTCCCGGATGGTGAATAATGTTCCGGACCTAGATA/C/GJTGACGA AGGTAGCACGACACTGTGAGTGCACTAA
UTR- 04350	125 C G ---	---	---	GAAATAAACTAAACTGCAAGCAATCAGTGTTAATAAGAAATTGTTCTTCTGTTT/C/GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCATGAGGTCTCAGAAATGCGGGCAAA CTCCTCTGTGAAATGTAT
stSG1026	55 T C ---	---	---	GTATAATTGAGCATAAGCCAAAGCCTTTTAAATAACCAATACTATCATTTTATGAAATCTTTACA AGAT/GJAAGCACAGTAGTACAATAATTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1028	70 T G ---	---	---	CACCTTAGATATGAGGAAATGGTTTATGGACACAAAGGAGTCAAGCTTTGGAACCAACATAG TTTCAACACAGTTGAAACCATGTGTTTGATATGCAATAACAGCAAAATAATTTTTCACCTC/CAJTTG TCAATGCCAATGCATTGAAAGGCCAGAAAATGAGAAAAGGATAACAAACCTTTTGATAAAAAGGTA AGAATTTCTGTGTG
stSG1031	128 C A ---	---	---	

stSG1033 1b	116 T C ---	---	TTTAAAGCTACATGCTGAAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCATTTCGG GCTCCAAACCTGTCTAGGAAGGCTAGACCTCAACACCAACACCTCCATTCGCAATTCCTCTTTGG CTACTATGCTTTTCCCTGACTTCTGCCCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1033 1a	107 A T ---	---	TTTAAAGCTACATGCTGAAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCATTTCGG GCTCCAAACCTGTCTAGGAAGGCTAGACCTCAACACCAATTCACCTCCATGCATTTCCTCTTTGG CTACTATGCTTTTCCCTGACTTCTGCCCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1243 b	225 GA ---	---	ATTGGCAAATGGGAAATGACACCAATCATTGATTACAGAAATGGTTTTATAAATCCTCCTCTTG AAATTATGTTGAGGCCAGCATGTAGCTTATGCTGCAATCCAGCACTTCGGGAGGCCAAAGGAGA AGGATCGCTTGAGCCAGGAGTTGACACAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATTCGTTG/A/AAAGTATTTTCAGACCAAAAGGAGGT
stSG1345 b	60 GA ---	---	AACTGACGTATCAGAGGGGCAAGTATCTCTGTCATAAATTTGAACCTAGTTGCTTCTTAC[G/A]CGCT TCACATTTAGCATGGGCCAAATTCAGGAGATGCCATGTCATAAATGGGGCAA
stSG1345 a	54 T G ---	---	AACTGACGTATCAGAGGGGCAAGTATCTCTGTCATAAATTTGAACCTAGTTGCTTCTTACGGCT TCACATTTAGCATGGGCCAAATTCAGGAGATGCCATGTCATAAATGGGGCAA
stSG1385 b	117 T G ---	---	TTAATGTCATCCAGGAGGGGCCAGGATGGAGGGGAGGGTTGAGGAGCGAGAGCGAGTTATTT TGCGTGGGATTCACCACTTTCCCATGAAGAGGGGAGACTTGGTATTTTG[T/G]TCAATCATTAAGAA GACAAAGGTTTGTGAACCTGACCTCGGGGGGATAGACATGGGTATGGCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCTTCTGTCG
stSG139	69 T C ---	---	TCGTCCTCTTCCAGTCTCTGCCAGAACATCCCATGATGTTGTGACCGCACAGCACTTTGTGCT T[C/G]CTTTGAGCACTTGCCACTCTGGCTGGTCTGCTGCCACTGATTGTGTACTGTCTTGTGCCCC GATCTGTTCCAGACAAGGCTGATTGAGAGACTCCACGTGGTCAAGGCTCTGTTTGTCAATCCCT TGCTCTCCACTTCCAGTTGGCTTCTGTGCTCATTCAGTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTCACTGCTCTCAGCTTGGAAATCCAGCAGCAAGAGATGTCCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1427	103 T C ---	---	CCCTGGAGTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTAGGTCCJA/GJCTCCCTTGCATGA AATGTGGGAGAGGGAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1471	50 A G ---	---	CAAAACCAAAATCCTCCACGATATATCTATTTAGTCTAAGT[C/J]TTTAATTCAAAGGTTGAGA ATGACGAATTCAGAAATTTCTTTCATACATAAATGCTTTCCTTAGTTCTGCAGATGGTA
stSG1483	44 T C ---	---	CACACCCACAAGTTTCATGCTAATGCCAAGTATCACTCTTGAGGACAAGGCAAAACCCAGTGTGCA [C/G]AATGTGGAGGATGCTGTGTCAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAAGAGGAA AATGCCTGA
stSG1696	67 C/G ---	---	

stSG1847 b	95 G A ---	---	TTGAGACAACAATGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAACCAATTAATAAATACTTGATCACTGTGCT TCAACACAACCTG
stSG1847 a	49 C A ---	---	TTGCAGACAACAATGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAACCAATTAATAAATACTTGATCACTGTGCTG TTCAAACACAACCTG
stSG1897 a	83 A G ---	---	CTTAATGCCCTTCTCTCTCTGACAGGAGACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGACACAGGACTT[AG/G]CCCAACACCTTCTCTCCCGGCTCCCAAGATGACT
stSG2022 a	86 T C ---	---	TGCTTGAGGTTTCAAACTCTGAGATATCTATGGCAAGTTTATAAAAGTACATTTGATCAAGGTACAA TTTTAACATTAAATACAT[C/A]TTCCATAATCTCATCTATTTAACATTAAACACAGGCCTTTGTGT TGTTATTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGGCTCAGTTGGGGGGTTGAC T
stSG2076 a	104 C G ---	---	AAACGTTGTCCCAAAATTGTTTCAGTTTCACAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAAACACTTAAGAATATATTTTACATT[C/G]ACATCACAGTGGGGCATTTT
stSG2108 c	71 A G ---	---	TTGAGCAACAATGATTGCGAATTGGGCACTCCCAACCAAAATGATTGAGGGCTCCACAGAGA GAGC[AG/G]TAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGTCTGA
stSG2108 a	49 T C ---	---	TTGAGCAACAATGATTGCGAATTGGGCACTCCCAACCAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGTCTGA
stSG2141 b	173 A G ---	---	TTATTCAGGGGACAAGCTGCACAAGGAATGTTCTTCTATTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGAAATAATCTCAGAATGGCAGCACCACCTGGCATGGCATGGTGCAGGTGGGT GCAGTCCCTGTGTCTTATTGCTTGAAGAGAGAAAG[AG/G]AAGTTCCCTATTATTATTAATTAAAGGC AGTTTTCAGAGCACTGGCATTCTTGTGTCTG
stSG2141 a	113 C T ---	---	TTATTCAGGGGACAAGCTGCACAAGGAATGTTCTTCTATTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGAAATAATCTCAGAATGGCAGCACCACCTGG[C/T]ATGGCGATGTCAGGTG GGTGAGTTCCCTGTGTCTTATTGCTTGAAGAGAGAAAGTCCCTATTATTATTAATTAAAGGC AGTTTTCAGAGCACTGGCATTCTTGTGTCTG

stSG2148	50	A G ---	---	TGGGAAACAACCGGCTATAGTCTGAGTCATATTTTAGACCGTGATTTC/GJAAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGTATTTTCGATACCTTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68	C T ---	---	CTCAATGAGGACTCCATCAGCCAAAGCGTTTATATGGCAGATGAGCTGCTACAAATCTGTGTGTGCT IC/TGCGCGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACGAGCCAGCCACCTTTTCCAT ACCTGGCAGAGGAAAGGAGTGAAGGACCA
stSG2189	41	C T ---	---	CAAGTGTGAAAGCTGGGATTTGAGCCTGATATTCACACTA/C/TCTACATTCCTCCAGTATAATA GGAACTCATCGCTAACTTTGAGCACTTAGTGTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGCGAAC
stSG2200	49	T C ---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGCTGTTCTGTATGATG/T/CJTTTATATTATGTAT AATGTCCTTACCTGATGATACCAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85	G T ---	---	CATTTTCGCTCCTGCTTCCCAGTACTACCCGCTCCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAG/GTAGAGCATCTCTCAGCCCTGGAAGACAGTGTGGAGCTTCAGCT
stSG2257	65	A C ---	---	TCAGTGATTGTAGGAGCTGGCTAAGTCATGTCTAACTGTGAGGCGAGGTATCAGAAGGGCAG/A C/TGTGAGGAACTCTGCAAGCACTGGGCTGTCTCCTCAGGCAGAAATTTCTCCT
stSG2306	67	A G ---	---	GTCATCAGCGTAGAGGTCACTGGTATAAACAACAGTAGCTATATGATATTTGGGAACATATTTTACA /A/GTATGCTCCCATTTGGGTTTTCCAAACTGATACAACCATGAGGTGAACACTTTCAGTGTTCACAG TTCTCCAGAGA
stSG2334	70	T G ---	---	GAAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAATAATCCCCGCAAAAAACA AAAAAT/GTGCAGTGGAGGGGCTGTGGAGGGGTGAATG
stSG2339	63	T C ---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAATTTGCTTGACTGCGAGAAGTAAGTGTGTACAC/T/CJ GTTCTCAGAGTCAACATTACGGTGAAGTGTCTATTTGGCTGTCTCCTATTCAATCA
stSG2465	76	C T ---	---	CAAGACTAAGAAAGCGCACCCGAGTGTCCACTCAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA/C/TTACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTCAAAGTGTGGGGTATGCA
stSG2549	140	T C ---	---	TTGCAGGCTTGATTTCCACAATAACAAGTCATGTATAGAGAATGTGAAATGATACTTGAAACCCAA GATATATAAATAATTGAAGTCATTTATGCTTTTGAAGTGGTTAAATATGCAAAAGCAGCTAAAG GAATATT/CITACACCACCCACCCCTTTTAACT
stSG2577	123	T G ---	---	AATTGCCAAATGGAAATTTCCAGAGGATTTTAGACCAACTTTGCCCTGTTGCATTTCCAGTTTGGT CCCAATATAGGCCTTCTGCAAGAGAGATCAATGCCGAACCGAACTGTGAAAGCA/T/GJGAACAATC CCGGCCAGATTAAATTAT

stSG2577 a	121 C T ---	---	AATTGCCAAATGGAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTCCTGTCATCCAGTTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAG[C]/TATGAACAATC CGGGCCAGATTAAATTAT
stSG2700	58 G A ---	---	ATCTCTCGACTGCTTTAGTGGGAAAGGAATCAATTTATTAAGAACTGTCCGGCCCC[G]/AJAGTCAG TCAGCGTTTGGGGAAATAAACCACTGTCCAGAGCAGAGGAAAGGCTACTTTGAGCCGGACACCA
stSG2724 b	101 T G ---	---	AAACAAGCTTTGTGATTTTCCACTACATTTTGTGTGCTTTTATTAATAATTTTGCAAATGCTATAAT TTAATACTTATATCCAATTGCTTGCATAATCA[T]/GTTTTTTTAACTCTGGGTGTTGAAAGAAC
stSG2776 a	65 G A ---	---	GTGGCGATCTTTACTTTTCCAGAAAGGCGGTAAATAAAACCTGTAGAAAGTCTCGAATATGC[G] AJTATTGGCCCTTTTGAGTTAGCCCGAGGAACCTCAACAAGGACACTGCTGGCCAAACCACAAA ATATCCACTAATTCGGAATATAGTAACCTGTCTGTCCGAATG
stSG2791 b	109 G T ---	---	AAGAAAGGTGGAGGGAAGGGAAGAAATTACAATGTTAGAAAGAGCAACTAAAGATTATTTC TATTACTTCTGAACGGTAAACTAGCAATTTTAAATAATTTG/TGGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 a	100 A G ---	---	AAGAAAGGTGGAGGGAAGGGAAGAAATTACAATGTTAGAAAGAGCAACTAAAGATTATTTC TATTACTTCTGAACGGTAAACTAGCAATTTTAAATAATTTG/TGGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
			CCGCAATTTCAACACACATCTATGAAACTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAACAA[C]/TGAACAAAAATAAGAAAGAAACCCATGAATGCCAGGTTTA ATTTTTTCC
stSG2826	85 C T ---	---	ATGGGTGCATTGTAAAGGCCAAATTAATACATTTTTCAGGCAGGGGCTGGCAATTTAATGAGCTGA TGTGTCCCAAGGGAGACGGCC[G]/AGGCTCACACATCCCATCAATACTCCTCCCAT
stSG2850	88 G A ---	---	ATACTCACGGGGCTGAAGGCAATGTGAAGAGTGAAGTCAAGTCTGGCAITTTTCTGTGGTGTGAGC AAAT[C]/GCCCCCTTTATTTTAAATGATTCCAGACATCTGGGCAGCATAGCT
stSG3031	71 T C ---	---	GTCCCAACTCTCTCTCTTAGAGAAAAAACTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAGTCAAAAC[G]/ATGAAGAAGCATCAAGCCAAAAAGGCAAACTGGGTGAGGC
stSG3058	81 G A ---	---	CAGCATCTCCAGAACATCTCCTAGAACTGAACCATCTTGTGCTACTATTGAAACAAAGCCAAGTTC CAAATCCAAAATAATAATGAACGTGCT[G]/GATAAACATTCTTCTATGGTTCCAGCCCCCTACTTT AGTT
stSG3092	94 T G ---	---	AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATTGTCAGTGGAGTC[G]/GTGGGGTGTCTAAGTGTCTGAACTGAAGTAG
stSG3230	95 A G ---	---	ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCAGGGGCC CAGGTATGTAGAGGCCAGTGGGGGTGGCCACTGTGGTGTCTTACCAACCCCTGCCATCCAGTCTG GCCCAGTACCTACCTGGGAGGTG[G]/GTGACTTGGCTTAAGTACTTCAATGCTTTAT
stSG3245	160 G C ---	---	

siSG3265	42	T C ---			AGGTGAATGAGTTACTAAATGTAGCATTTATTTATAAGGAAT/GJGCAATGTGGAATAGTTTCTCAG TTTTCAATTATGGAAAGATGATGATTTTACGCCACATTCAGTGTATGTTTCTAATAACACAATCGAC AGGACTGTCTGTTCACTACAAATGGAGGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGTCTTGTCAGCTGAATTTCTTGGGCTTTATGTGGCAGTGTGTGTAATAA
siSG3269 b	141	C T ---			TGTACTTACTGTGTCATCCTATCCATTCCCTCCCTGAGCCTGGAGCTGCTTCCAAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAGTTACCCCTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA/C/TTGTAGATCCCAAGTCCCTGACACATTTTCTTAAGAAACT
siSG3269 a	24	A G ---			TGTACTTACTGTGTCATCCTATCC/AGJTTCCCTCCCTGAGCCTGGAGCTGCTTCCAAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAGTTACCCCTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTAAGAAACT
siSG3284	130	C T ---			TTAACTCAAGAACTTTCAGTTACAGGAAGATTTATCTAATATTAAATGACTAAATTACAAAAGC ATAAATGTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCCA/C/T TCCCTAACTTTTGTTAATTGCTGTAAATGGGACATTTGTTGTTTGTATCTACCC
siSG3292	99	A T ---			GTCTCAAGTGAATCTGTAATAACATTTTAACTGCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA/TTTACAAATCAAAATAGCATTTTTCCTAACTTCAA TAAATGTCATATCTTTAGCTCTCAGTTC/AGJCCAGTGTATOCATTTTCCCGAGCCGTAGAGCTTTTCTG TTTCTGTAGATTTGCTGTGCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTGAGCTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCTGCTCATGCTTTCATTCCTTTTAA GATCCCCAGTATATTTTCTAAATTGAACCTGTTTGTGGAATAAATAATCTGAGGACCACTCAGAG GG/C/TATAAGGGAACCCCTCTTTGTCTTAGTTTATAAGGACTTTCT
siSG3369	69	C T ---			CAAGACTGTAAGAACGTAGGCCCTTGTGAGAGTGAAGGAAGGATGCTCGAACTTGGCCAGGACTCAGG CTTCAGCTTCACAAATCCCGAGGAAGGAATGACATTTCCAAACTGTCACCTTTGTAGC/G/TCTGGGT CAAAGTCTAAGAGGACAAATAAATAGAGACT
siSG3398	125	G T ---			TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCAG/AGJCTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCCAGCTCAGCCAACTGAGTAGCTGGCTGCAGGACAAGTCAACCATGCCTA CCTAAGTTTTGTAGAGACAG
siSG3416 a	43	A G ---			GTAAAGACAAGGTTTTGCTATGTTGACCAGGCTGGTCTTGAACCTCTTGGCTTCAAGCGACCGTACCA CCTTGGCCCTCCCAAGTTGCTGATATTACAGGTGTGAGCCAGTGGCCCGGAGCTTTTAACTGAAT GTTGAAATCAATCTGCTCTTTGCTGGGTAACACTGA/T/CAAGTTGCTTAACCTTTGTGAAACCAC TTTCCCTTATCTGTAACAAAATGGACAACAGAACTTTTCCCTTTCCTCTC
siSG3424	173	T A ---			GTTTCATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTGAGGTGATGTGATGGAGGCTCACAGA ATGAGTGGCAGAGAGGGCCCTT/A/GAAATAGCTTACTCTGTTTTCCTATC
siSG3436	88	T A ---			

stSG3463	103 C T ---	---	GATACAGAAGATAGTGTGGTATGGATAGTATGAAGGACAAATAATACAAATATATTTATTG AAATAAACAAATAATGCATACACAGCTCAATGGTGCAC[CT]TGGAAACAAACTTGGCTTGACTATATTA CTGA
stSG3491	71 G A ---	---	CAAGATACTTCAATGCTCTAAGTAGTGCAGTCTGGCAAAATATTTCTACGAACAAGGACGATTG AAGA[G]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTACTGGCACCTGTGGATTTCTATTAACTCATTTTATACTATTTCTGTGATG ACAGAAATAAGTTAAC
stSG3523	33 C T ---	---	TAGCCATCTTACTCTAGTCTTTTGGGTTTTC[CT]GCATATATGTGTGTACAAACACACACACACC CCTAATCTCTCAATGCTCTTGGCATAAGTTTATCTCTACTGGTCTC
stSG3536	213 A G ---	---	AGTACAAACACAGATTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGTAGCCTACCTACACAGCTGCTACAAAACCAAAATACAGAATGGCTTC TGTGATACTGGCTTGTCTGAAACGCATCTCACTGTCTATTGTTTATATTGTTAAATGAGCTTG TGCACCATTAG[G]TCTGCTGGGTGTTCTCAGTCTTGCCATGAAGTATG
stSG3583	112 G A ---	---	GAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]AACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586	60 G C ---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGGTGGTG[G/C]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGGCCATTGCACTCCAGCTTGAGACTGTTTCAAAAA
stSG3589	101 T C ---	---	ATATAGTGTGTAGCATTATAAACTCCTTTAAAAGCAATCTGGCCATATCAAAGGCCAAAAAAGT GTATATACCACCTTGGCACAAAAAACCCCAATGA[T/C]CTATTTCGAAGATGTATCCAGATGAAA GTATCCAACAACAAAAAGCTATATACAC
stSG3590	70 A T ---	---	GAGAGATGAGCTATTTATCTTTTACTTAATGAAGATGTAAGAAATGATCTCTGTTCTAAAAAAA AAA[A]TTTCTCTGATGTCTCTTGACCCCTGTAGGAACACATTCAGTTTCTACACT
stSG3619	78 A C ---	---	CAGTGAGACTTCTCATTTTATAGCAAAATACATTTTTCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATTTACJAAACAACCTCCAGAGAAAACCTGGGCTCTATATATTTAAG
stSG3644	40 T C ---	---	ACATATGTAACGTCCATTAGTAGCCATATTTAGGATGAGAT[C]GGATTGAGAGGCATGAACCAAGG ATGCGTAATAATCATTTAATAAATAAGTTATCTGGGGGAAACGGCCATTTGTCCAACATTTACTAA GTGCTACTA
stSG3646	70 G A ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGCTTACT GGT[G]ATATTAACCTTGATACCTGGTTAAGATGGTGTCTGTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATA/A/GJTATGCTTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43 A T ---			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG/A/TJTGATAACAATAATATGCTTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85 A C ---			ATTGTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCGATGACCATCCAAACCTGGACTCACT GAAATATCTACGAGGC/AC/TTCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3693 a	30 C T ---			ATTGTTCCCTGAACATTCCCGTGGTCTCC/C/TJCTGAAAGCCGATGACCATCCAAACCTGGACTCA CCTGAAATATCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3698 b	145 G A ---			TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCCAGGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCAGATTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG/G/AJAGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---			TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCCAGGGTTG/C/GJTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGAAATACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107 C T ---			ACCAGCCTCATGTGCAGAGGGTCTCTGCTGGATCCCAACTGGAGCCATCCCTGGGCCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTAGTGTGAAG/C/TJACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGT
stSG3725	104 G A ---			GCCAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAATATATTATTACAGCCAAACAGCAACAGCCCG/G/AJAGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
stSG3751	128 G A ---			CGGAAGAAAGAACACAAATCCACAGGAACAATCTATGTTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGAGGGGAAAGAGAGAGGATATGTTCCCG/A/JTT GCTGACTCCATGTGTTGCAAGAG
stSG3787	49 T A ---			TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGGAGTCTCTTAT/JAAAGTTCCTAAGA CACTGAGGGCATAAACCAACAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCT
stSG3880 b	115 G C ---			GACAAGAGGGAAGAGATCGCCAGAGACAGGGCTGGGGCAGCTGGGGGTCCCTGAGTGCCAGGGCGC CACCACACGTCTGTGGGTCAAGGCCCTCTCTGCGGAGCAGGTCTA/GCJGGCAGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCOCT

stSG3880 a	36 G C ---	---	GACAAGAGGGAAGAGATGCGCCAGAGACAGGCGTG/CJCGGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGGCCCTCCTCTGGGAGCAGGTCTAGGGCACGGAGGATGCAG GGCTGGGAGGGACCCACCTCGGGGACCCAAAGGAGTCCATTTCTGCOCT
stSG3895	44 A G ---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTG/A/GJT/TTTTTTTCCATTAACTAA TACATGCOCTCATAGATATATTCAAATTAGTGTATACCATGGGAACAAGATGCTGATTCGTCAACTG AAAAAT
stSG3902	104 T C ---	---	TCTGTTGAGACTGGAGAGACAGGTACCAAGCACCGACTCTGGTGGGAACCTGGCTTCTGTATAACA TCATCTATTTCACCTAAATGTGAACGTCTTCTTTCT/CJTCAGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTTGCTGGACAAT
stSG3935	50 G A ---	---	GGGTGCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC/G/AJCTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCAACAACCTTCTCGACGT
stSG40	25 A G ---	---	GAGGAAGAGGTTGAAGAAGTGCTGA/A/GJAAATATATTAGATTTCTTGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAATAAGGAACAATAAACCCCTTGTGTATGTATCA CCCCAA
stSG4009	32 A G ---	---	GTGTGGGCTGTCTGATGATGAATGGCGGCTC/A/GJACTCTTTACGGTCTTACACTTTTATGCTOCT ATGAATCTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGGTTTCCACACTGCTTACA
stSG4033	123 T C ---	---	AGAAAGCCTTGGGACAAATGGCAGTGCCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTT/CJTGTAAC AGGTGGGCAACAC
stSG4038 a	29 G A ---	---	GCTGAGAGCAGTGTACAGCCACGCCCTGT/G/AJCGCAGGCCCACTCTGTGCAATAAACATGTTCTGOC CATGTTCTCAGTCAGGAGGTTCCAGGCTCCCGGAGAGCACCTGAGGGTTCCATCACT
stSG406	53 T C ---	---	ACTGTGGTTCAACAGTATTGCGTTGTGACAGTGTGAGAAAGCTAAACGAACAAT/CJGGTTTTAGTT TTGCTGAAGACTGGCCTTATTAAATGGACAGCTTTCTCAAGAGATTATAACTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55 G T ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAAGATACTATTGTCTGTAGATGTATTAG/G/TJATAAAAA GTTTGCTTCTGTAATACCTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCTTTGACTAACCCACAGGCGATTGCCCTTCATCCTGG
stSG4095 a	27 A C ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAAGATACTATTGTCTGTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAATACCTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCTTTGACTAACCCACAGGCGATTGCCCTTCATCCTGG
stSG4120	65 G A ---	---	TGCATGTTCCACATCTTTCATAACAGCAAAATGTATAATAACTTACGTACTTATGGAATAATCAC/G/ A/C/T/T/T/C/C/C/C/C/CAGAGAGGCCCCACAGTTAAACACGTTCCAGCACACCACTTAATCCACCGAGCT

stSG4128	54 A G ---	---	CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTCCTTTGTGTACATTTCTTJAGJTATATTATTT TACTTCTCTGAAATGCCACATAATTTGCAATAAATGATTCACTCCTTAGCTCCAAAGCAAGTCCTC TTTATCAAAATGCAAAATGTTCCAGAGGG
stSG4209 b	128 G A ---	---	CACGAAACAGATGCAGCCTACACAGTCTGTAGGACCGAGGCTCACAACATCCACATGGCACAAAGC AGGCCGGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTCQ[G]AGC AGGGGACCACGGAGGCGACAGGTGCTTTGATGCTCCGAAAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---	---	CACGAAACAGATGCAGCCTACACAGTCTGTAGGACCGAGGCTCACAACATCCACATGGCACAA[G] /A/CAGGGCCGGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTCGGC AGGGGACCACGGAGGCGACAGGTGCTTTGATGCTCCGAAAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---	---	CATTACCCAGAACGCCATTGGAGGACCAGAGC[G]ACACGGCCGGGACTCCCGGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGCCGGGGCTGCTCTCCGCCAGGGCGACAGCTGAC TGGGGGACCATGGCCGAAAGAGGAGGATGACCGGTCATG
stSG4301	81 T G ---	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACTTTCCAT TTAAGCAATAAATT/GIAGCTTCTGAGTAGTTGTTCCAGTTTACCCCAACATTTTG
stSG4331 b	71 T G ---	---	CTCAGAAAGGCCAACACAGAGAAAGATACAAATACATTTCACGCTAATATTTAGTTTATGACAC AGAGT/GJTTTTCAAAACAAGTTTAAGTGTCACTGAAGAGCATGTTAAAGTTTAAGTTATCATT GGAGAGCAGATTTCTGGCCTCGCCCTTGTGATTCTGTTTGGGGGGTGTC
stSG4340	76 G A ---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAAGTCAAAAACC ACATGTTCTC[G]ATTAAGTGGAGATAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109 A C ---	---	TTCCCAACCATTTAGTGACAGAGCTCAGTCATGCAAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTTCTTGGAAATTTCCATAAGGGATAAAGTGCATCTTTTGC/A/CJCTTCACAACCTAGAAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTGAGG
stSG4361 a	24 T C ---	---	TTCCCAACCATTTAGTGACAGAGCT/CJ/CAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG CACAAGTCTTGGAAATTTCCATAAGGGATAAAGTGCATCTTTTGCACCTTCACAACCTAGAAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTGAGG
stSG4376	73 A G ---	---	TTCACTGCTACTGGTTTCGGTGTCTGAGTCCCTCAAACTCTGCTTTGCAAGTGTCTTCTCAAGGGGAG AACAG/GJCTGGAACCTCGGGCTCTGCAAGAAGCCATTCTTTCCAAGCCATTCTTCTCAGCTGC
stSG4381	50 T C ---	---	GAAAGCCACAAACACTCCATAGCCAGAGAATGACAACATACGATTTCTTJ/CJTCAGTCTTGTAGT ATCCACAGTAGTGATGCTGTCCATGTACAAGTGTCTGTCCAGAACACCCATTAAATTCCATGCC
stSG4410	79 A G ---	---	ACCAATGGTTCTGCTATGTGCATCCGATATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAACACCCG[G]GJTGACAACGAAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGCTTGT CAGCTGGGT

stSG443	65	C T ---	---	AGCAGATCAGTCAGCCACTTGCTCTCTCTTTAGGGAGAGGCTAGGCGAGTGAACACATCA/C/
stSG4430				TGTATGCAATGAGAAAAATAACCAACTGGTAGGATGGGGAGGGAGGGAGGCAATAGGCAC
a	54	A G ---	---	AAATGGAATTCATCTCTGGCTGTCTCTCAGGTC
stSG4448	99	G A ---	---	ATGCACATTAAATGAATGGCCTAACTACTGGAACCTTTAGTAGTTCTATAAAGGT/AGJATTAAACATA
				GGTAGGATCCAGTTCTATGACAGGCTGCTGAAGAACAGATATAGGCATCAAGAGGGCCATTTT
				CCTCCCTCCCTTCTCTTCCCTTCCAGTCTTTCCATAGTGTTCCTCCCTCCGCCACCCAGGCTCT
				CGCTAGCCCTGCCCTCTGGGTCACTGCG/ATGGGTAGGCCCCCAAAAA
stSG4449	92	T C ---	---	ATTAGCCATTTCATCTTGCAACAATTGCTTTACTGTAACCTAAGAGTACTGTACTGATGATGTTTACAAT
				TAACTTTGGACAAGTTAAACCTTA/CTTAGTGACATTTCTGTCTAATAATCAAAATACCTTCATCATA
				GGCTGAACATAAATTATTAAGAGCAAAAGTTACCCCTCC
stSG4467	42	C A ---	---	CAGACATGAGGGATGGCCCTGCTCTCTGGACAGAGCCCTCA/C/AGATGATGTCCATGTTTGTGT
				GAATGAACCTCAACACTCTTCAGTTTCTAGTCACTTTCTGTATCGAGCGACACACCGAGGAG
				CACACCTGCTTCCAAAGGCTGCTGCTCTGTCACACAGT
stSG4475	21	A C ---	---	ACATGTCATTTCTGACCAGG/AGJATTAAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGA
				TTAAGAGACACAACTGGACTTTTGTCTCTTACTGTAGCACCCAGGTTTCAIG
				GTAACATTCTGGGGTGGGTGAGACAAACA/AGJATGAACCAATAATTAATTAACAATTATACATT
stSG4477	32	A G ---	---	TCAAGGAGACTTTTAACTAGTTAATGTGAACCGCAGCCATCAATGTTTGTCAAGGAAAGGGAGA
				TGAAGTCTTGCTCTGGGGCAACGTTTGGCTCTATTCAGTCAAGCTTGGC
				TGAACAGAGCTGGTGGGAGCTGCAGCGAGGGAGGCTGGGGCCAGATGAGCCGGCCGGGA
				CAGCAGGCTG/C/TCACAGCTCTGGCGTTGGTAGAAGAGGACATAGGCTGCCCTTGAGCTCGATCT
				GATTCTCATTGACAGGGGAGACGCTGTGTCTCA
stSG4531	79	C T ---	---	TGCATTAAAGGAATGATACGGCATA/TTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATT
stSG4550				AAAAGAGACAGTGGGCAC/C/CAATTGGAGGGGAAGCGGGGCAGGGTTTAGAGAAC
b	86	G A ---	---	TGCATTAAAGGAATGATACGGCATA/TTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATT
stSG4550				AAAAGAGACAGTGGGCAC/C/CAATTGGAGGGGAAGCGGGGCAGGGTTTAGAGAAC
a	85	C G ---	---	AATCAGGCACAAAGCTCGGGAGAGAAGCCAAAGCTCTCTGCAC/AGJATGGGAGGGAGACAC
				CATTGAAAAAGGCATCGTTCTCTTCATGCAAGCGAGGCTGGCTCCACAGGCATGGTCTCTTG
stSG4590	47	A G ---	---	AATCTGTATACCCAGCGCTGGT/C/CAATGTACTAGTGTTCACAGGATTTTATACTATTTC
				CTATAAGGTTTATCATGAATAAAAAGCTCACAAGTCTTTTCAGCCATTGCAGATTTCACATTATCT
				TAATATCTCTGTTCAAGATGCTCTGGAG
stSG4623	22	T C ---	---	TAAAAAAAACAACCCCCCAAAAAACACCCAGAGTTTGTAGTTTATGTTTTCAGATTAAAG
				GTATTTCTTTCTAGCTCTAAATTTTGAGTCA/TC/ATCAGAAAGTCTTCCCTACTCTCAAGGTGA
stSG4843	102	A C ---	---	GAAAGGA

stSG4850 a	38 C T ---	---	GGAACTAAACTGGGAATGCCGAGGAGGAAGGGGCTC/TGTCACCTTGACAGCCACGTCAGGAG AGCCAGCGGTGCTGTGGGAGGTTTCAAGGTGCTCCGTGAAGAGCATGGCAAGTTGTCTGACAC TTGGTGGATCTTGGGTCC
stSG4879	86 A G ---	---	AACTCTGAAGGGGTGACCTCAACCAGCCCTTGTTCTGTGAGGTCTGCTTTTGACAGAAATGGCCTG CCTTGGGACTGGAGCAG/GAGCTTGGGTGAGCTCTAGGTGAGGGTGTGGAGGGGCATAGAAAT AAACCTTC
stSG4885	104 G A ---	---	ACTGGACTGGCTCGCTTCTGAGCCGGCTGAGCGGCGTGCGGACTGCGGGTGACCACTCGCTCTTCAG AGACTGCGCGCGGTGACACGACTACGCTCTGTGGGAAAGCAGAAAGCAGGACC
stSG4896	112 C T ---	---	AAACAAATCAAAACCCCAATCCCAAGCAGTCTATGTACAGGGCCACTCCCTGCTCTCTGCCATAGAG GGTTGGGGGCGAGCTGAGGAGTGTGGGGCTGGGCACCTTTCTCTGAGCCACAGGCCCTGAGG AATTAATTGACTG
stSG4932	22 G A ---	---	ACAGTGCCGATGGTTACACAAT/GAJTTGTAATGTATTTAATCCCACTTACGAATGATTAATAATGA TAAATCTTATGTTATTTTCACTACTACCAAAAGGCTGTGGTGCGAGGGTGTGTTCTGTGCTCT
stSG4950	24 A G ---	---	TCATGACTCCCAAGAAAGGTCT/GAJTCTTAGCTTCCCTCCCTACTTCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGCAATGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A ---	---	AGATACGGGCAAAACACTGGGATGGCTTCTGACAACCTTAAGAGGTCTCCAGTTATTTCTGGGT GGGAACACTGACCCAGCCTTATTCCTTCAAGACTCTAGTCATTGGCAAGGAGGATTCATGAGCC CC/GAJGTGACACAGATGGGGCCCTGCTCTATATCAAC
stSG4961	91 C T ---	---	GAAGGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAAGGAAAGTA/C/TJAGAGAGGGCATTGAGCCCAAGTCAGCAACACAGACAA
stSG4967	72 A G ---	---	ACTGGTCCCTCTCAGCAGATTGAGGGTGTGTCAGGGCTGTTACCAAACTCAGTAGGAGTGCAA GGGCTT/GJTAACCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCTCCCTTTTCTGTGTGC AACCTTG
stSG4997	22 T C ---	---	CAAGGAGAGTAGGAGCCCAAT/CJTITTAATGGTTTCTCTCCCTCATGCTATTTGATCCAAAA CTATATACAAATTTGTAGCAGTCTGTATAGTTATTACACATGTTTAGAAGGGAGGGAGGCAAGAA GGGATAGGAGAGTGTGATCCAAAAT
stSG6312	37 C T ---	---	ACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA/CJTATGCCATGCGGGAAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCAATGAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107 G A ---	---	GCTCTGGTCAAGCAAAATCTCCAGGACAGAAGCAAGGACAGTAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTGTCCAC/GAJATAGTTGAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAAACATTTGCTCTTTGGCCTGGTGTGGACAGAAAGGTGGCCAA ATGGATTGAGTATGAGCAGACATG

stSG8362	88	G C ---	---	TGTGAAATGTACACTCAGGTCTAACAAATACCTATTATTCTCTGGTTAAGAAAGGTTTAGCAGGAGCCTCCAATGAGCACTGTATGTA[G/C]AGAAAAGGGAAGGAGCAGGAGGAGGAACAGATCTGCACAGAAT
stSG8010	62	G T ---	---	CACATCTGTGTTCTGGAGCAAGGGAACACAGAAAGCCAGGAGTTTGGGTGTGCACTGG[G/T]GTCTTTCAACTGGGTGGAACCAACTGAGTCCTTGAAGTCTCGCTCTGAGGCTGCAGAAAGATAGA
stSG8022	53	G A ---	---	AGTCTCTGACTCCCTGTTCAAGTGACGTCATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTATTACACCATGGAAACTGGAAACTCTACAAATCAATGCGTTATTCTTTATTTCAGAGGGCAGGTTTATCAGCACACGCTGATCTCC
stSG8032	67	G C ---	---	TGATTGTTAGGATAAGTGGCATTGTGTTTACAAATTACTTCCAAAGAAATTCAGAAAAATTGTGTGTTGCTGGAGGCAGGTAGCAAGATAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA
stSG8064	46	C A ---	---	AGCTGGCTTCTCTCTGTCGCTTCCTGGAGGCTTCACTGCTCG[C/A]CGGTGGTCCCTGGTGGCCGTCAGGACCAGGGGTGGAAACAATGCCAGGGAGAAATTCCTGTACATCAACACAGGGAACA
stSG8084	23	G C ---	---	AGCTGGCTTCTCTCTGTCGCTTCCTGGAGGCTTCACTGCTCGCCGCTGCTGCTGGTGGCCGTCAGGACCCAGGGGTGGAAACAATGCCAGGGAGAAATTCCTGTACATCAACACAGGGAACA
stSG8072	59	A G ---	---	CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGTGGTCTGCTGCTTAGGG[G/A]GTGGCAGAGGAGAAGGATCCGAGTATTAGTGGCCGATGCAGTTCAAGCTGTGCTGTTCAAAA
stSG8100	40	A G ---	---	ATACCCACACACCCCACTCAACCTTGATCAAAATCCA[G/A]GAGTGTAACATAAGTATAAGAATATCATGACTAGTTAAAGATAGCAATACCATAAGGTACAAGTTCAAGTATTAGTATAACAAGTATCTGAGTAACAAATGCTCTTGGAAATGGG
stSG8102	138	T C ---	---	AAGGCTCCTTTGAAAGCATGGTTATTGTTTCCATTTAAGTGTCTCAGCTATACTGAAGTATGATTGACAAATAAACTTGCATATATTGAGATGTACAGTGTGATGATACATGTATGTATACAATGTGAAA
stSG8105	110	A G ---	---	TGAT[CT]GTGCTAATCATATAATCAATAATTGGTATAATTGGTTTAGGAAATGTGATGGTCAGTGGTCTCAAACTCCAGCGTACACGAGGATGGCTTGTGCTTGTTAATACACAGATGACTAGGCC
stSG8130	96	T C ---	---	CACCTGGGAGTTCTGTTGGAGTCTAGGCCCTGAGAAATATTC[AG]TTCTAACAAAGTCCCAGGTGACCTGAGGCTCTGGACTGGGAACATGCTTTGAG
stSG8130	36	C G ---	---	GTGTGTACATCATTGGGAATGGAGGGAATAAATGACTGGATGGTGGCTGCTTTTAAAGTTTCAATTTGACATTCAGACAAGCGGTGCTGAGCCT[G/C]GTGCCCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8145	124	T A ---	---	GTGTGTACATCATTGGGAATGGAGGGAATAAATGA[C/G]TGATGGTGGCTGCTTTTAAAGTTTCAAAATGACATTCAGACAAGCGGTGCTGAGCCTGTGCTGCTTCAGATCTTCACAGCACAGTTCC
				TTGTGGACTTCAAAATTC[TT]CTTCAGATTTTAAATGACATTATGCATGTACATATTTTTAAAAATTTAGACACATTTTAGAGAACACAATTTGTGAACACAAATCTAAGAAATGAATGAGATGTTT[AG]CTGAAATCTGATTCAAAACACTTATCTTAAACTGACTTCTGTCAATCCTCTGCTGTGTAAGG

sfSG8145	97	C T ---			TTGTGGACITCAAATTCCTTCAGATTTAAATGACATTATGCATGTACATATTTTAAAAATTT AGACACATTTTAGAGAACACAAATGTGAACCTTACAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATTCAACACATTATCTTAACTGACTCTGTCAATCTCTGTCTGTGAAGG
sfSG8150	36	A G ---			ATTGTTCTTGCAATTCCTGGATTTTCAGAAATAGT[AG]ATAAATAAATACGGGAATCCTTAGGCAT TCGTGTTTTCTATGTTTTAACAGGATTTCTCTAATGTTTCGCTATTAAATACCATGCAGGAAATTT GGGAAAT
sfSG8340	30	C T ---			AGAGGATTATGGAGAGAGCTGGCAGGATC[CT]CAACATTATGACCCTGAACCTCCAGAACTGGAT TCACTAGAAGGAGAGAGAGAAAACGGCTCATCAAAA
sfSG8466	111	G A ---			TGTGTATTGGGTGACTGTAGCCTAAGGATAAATGAATAAATGACAGCAATGTTATAAGCAGTGGGA GGAGTGAACCTGGGAATACTTGGTTACAAGGTTTTCACACTACCT[G/A]TGAAGCAGCACAGCATTAT TTGAAAG
ESTD-ACE	--	-- -- --			GATCAAGCAGTGCACACGGGTACGATGGACAGCTCTCACAGTGCACCATGAGATGGGCATATA CAGTACTACCTGCAGTACAAAGATCTGCGCTCTCCCTGCGTGGGGGCAACCCGGCTTCCATGA GGCCATTGGGGAAGTGTGGGCTCTGGTCTCCACTCTCTGAACATCTGCACAAAATCGGCTGC
ESTD-ADA	--	-- -- --			ACCATCTTATACTATGGCAGGTAAGTCCATACAGAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCAGAGGCCCCCTGGGAAATCCAGGTCACCTGTTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGAGAGCCCTCGGCACTGAGCTGCAGADCC GCAGACCAACTCTGAGCTTCTGGGCTCTGAGTCTGTGCTC
ESTD-AK-168	--	-- -- --			GGGAGTGACAGCTAGAGCAACAAAGGGGGCTCTACAGCTGTGTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	-- -- --			AATCCAGCAGCTTTAGGAGGTGAGGAGGCATATCACAGAGGTACAGGATTTGAGACCAGTCTGA CCAAACATGGTGAAACCCCATCTCTACTAAATAACAAATAGCCAGGCATGTTGGTGCATGCCCTGT AATCCAGGAGGCTGAGCAGAGAAATCGCTTGAACCTGGAGGCGAAGTTGTGGTGAGCCGAGAT GGCACCATTCAGCTCCAGCTGGGCAACAAGAGTAAACTCTGCTTC
ESTD-ANT1	--	-- -- --			TCTCCTGTCACTTCTACTCATTAGTTCAAGGTGAGTGAAGAACTGGGGCAATTAACCAAGTAATTCA TGGACTGCCCAACTCGAAACAGAGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-APOA2	--	-- -- --			CCAGGTGTTGTGGCAGTGCCTGTATCCAGCTACTCGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGAGGCGGAGGTTGCAGTGAGCTGACATCGGCCACTGCACCTCAGCTAGGTGACAGAGCAAG ACTCC
ESTD-ARSB	--	-- -- --			GGAAGAAAATGGAGCCTGTGGGAAGGAGGCGTCCGAGGGTGGGCTTTGTGGCAAGCCCTTGCCTGA AGCAGAAGGGGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTGACGTGTGGAAACCATCAGTGAA GGAAGCCCATCCCCAGAAATTGAGCTGCTGCATAATATTGACCCAAAC

ESTD-C7	--	--	--	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	---	---	---	---	GGCAAGTTTTATTGATAGAGAGGAATCAATAATGGCAATGAGGAGACATCACTGGAAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCCAAACCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAG TAACATAATTGTGCTTCATTATGTTGCTTTCCCGGCTTCTCTCTCACACAC
ESTD-CB23	--	--	---	---	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTGATTATGTTCTTTCCCGGCTTCTCTCTCACACATACAGAGAGCCCTACAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAAACGTGTTCCCAACCGGA GGTCGCTGTGTTGAGCCATCAGAGCAGAGATCTCCACACACCAAAA
ESTD-CB24	--	--	---	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCATACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTCGTGTGTTGAGCCATCAGAGCAGAGATCTCCACACCCCAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCCGAACACGTGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGGTCAACAGACAGACCCGACGCCCTCAAGGAG
ESTD-CB25	--	--	---	---	---	---	GTTTCTTTTCAGACTGTGGCTTCACTCCGGTAAGTGAGTCTCTCTTTTCTCTCTATCTTTGGCGTG TCTGCTCTCGAACCCAGGCTGAGAGATCCACGGACAGGGCGGTGAGGAGGCCAGAGCCACCTG TGCACAGGTACCTACATGCTCTGTTCTGTCAACAGAGTCTTACCAGCAAGGGTCTGTCTGCCACC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCGGTG
ESTD-CB27	--	--	---	---	---	---	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAANAAT TGTTGTTGGGCTGGTTGCATTTTCAGGAGTGTCTGTGGAGTTCTGCTCATCACTGACCTATCTTCTGA TTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACGCCCTCTTCTCTCCACCCCAATGCTGCT TTCTCCTGTTCACTCTGATGGAAGTCTCAACACACCATTTCCATACC
ESTD-COL2A1c	--	--	---	---	---	---	AGAATGTATATAGTCTCAAACTGGGCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTGTCACCTTTCAGGGTGTTCAGGTGGAAAAGGT GAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCTTTTG GTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1d	--	--	---	---	---	---	TGAGAGAACACCTAGTCCCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTCTGGGACCTGGAACACTGGACTTCTTCTACTGACGACAGACAAGACTTACCC AAGAGAGATTAAATGGCAAAGATATACAATACAATTTTATTGACCAAAACACTATCATGGAACAGC ATT
ESTD-CPT2	--	--	---	---	---	---	GCCGCAATGCCGGGAGTTTCTCCAATGTGTGGAGAAGGCCCTTAGAAGACATGTTTGATGCCTTAGAA GGCAATCCATCAAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCACTTCTCTCATCATGAAAAC TGGGAGGCCGGGCATAGTCTCATGCTGTATATCCAGCATTTTGAGAGGCTGAGGCGGTGGATCAC TTAGGTCAGGAGTTTGAGACCAACCTGGCCCAACAT

ESTD- CTLA-4	--	--	--	---	---	ATGGCTGCTTGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTACCGAGACCTGGCCCTGCAC TCTCTGTTTTTCTCTCTTCATCCCTGTCTCTGCAAAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCGAGGCATCGCCAGCTTTGTGTGAGTATGCATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	CAGGCCAGCGTGGTCGAGGTGGTCACCATCCCGGAGAGAACAGGTGACCCACCCTATGCACAGGT TCTCATCTTGAAGCTGCTCTCAGGGTTCCCTTGGCTGAGCAGGCGGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	AAAAAACATTTTAAACACCTTTTCAATCATATACACCATAAAATTTCCATTTTTTTCACATAAGTCAGTT TGAGCTGAGTTTTTCCAATTACTTGCAATCTAAATGTCTATACTGATTAATGCAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAATATTACATATCTGGATTAAATTATGCCCATAT CTGCATGTC
ESTD- D17S33	--	--	--	---	---	CATCCCAAGCCCATCTCTTAGCCACTGGCATTTTTTCCCGCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCCCTTTGTAGTCCATGGGAAGGCTCCTCTGGGGGGTG GGGTTGTGTGGCTATGTGTGGTCTTGTGTAGACGGGGCTTTGGTTTCAGTTGCATATTGCGTTATT GCAGATTGCTTTGCTTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	TTTGAGACCACCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATACAAAAATTAGTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGGAGGCTGAGGAGGAAATTGCTTGAACCCA GGAGGCAGAGCTTGCAGTGAGCCAAAGATCACACCACTGCACCTTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	--	---	---	AACTGATTAGAACCTGAAATACATATTTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAATCCAATAAGTACACTGTATAAAGAAATTTAACAGAAATATCATTTGT TTATCAAACATTTATCATCTATTTTATTGGTAAGCCATACTAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	AGGTTCCACATTATTGCTGATGTTTGGTGTGTTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACTTGAGACGTACTTTTCAAAAAGCTCTCTACAGCCGTTGTTGTTATTAAATCAAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCG TGAGTCTTATTCAAAAGTGCAGGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCCG AGAAGTGAACATACCTGCTCTAGAACCCAGAGTCATCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	TTTTCTGTTTACCTTGTTTCAGATCCTTCAGAGGAATCCCTATATATGCGAGGTATATGAAATGTATTT CTTAAACAATAAAGTTGAAAGTCCAAAATTACTCCTTGATCCATGGATGCAGAAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGCATATGTTTCATCAGAGCCCTTGGGTGACCGAGGTGTTT GCCAATAAGCAGTAATATTTGAGAGGAATCTGTTTTCATGTCAGTAG
ESTD- D4S95	--	--	--	---	---	CTTTTCATGCAGATAGGCTTTCTCTAGTAATCACAGAAATTTTGAGAAGAGCAAAACAACCTTCAAGG ATAATGGGGCAATCACTTCTTCTCTTTAGAGTCTACCGG

ESTD- D7S399	--	--	--	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCTTTACAAAACATTTTCATCCATGGACTCCATACTAG AATATTTGAAGAAAACAAACATGACAAAACATTTTC
ESTD-DM	--	--	--	---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTCACGCTGCTGCTCAAGCAGCTGCTGGGCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCTGGGGAGAGAGAGGAGTGGGGAGGGAGACA GAATGCTGATTATCTGTGGAGAACCAAGAACTCTGGGCTGTGGGTAGGGGCAGCTGCTTCCAAAGACC TCTGATTTGAGGAAGGGGAGCAGAGAGCGAAGAGAAACAGAGT
ESTD- DRD1	--	--	--	---	---	TCCCAGCCCTATCGGTCTATTTGGACTATGACACTGACGTCTCTCTGGAGAAATCCAAACCCATCAC ACAAACGGTCAGCACCCCACTGAACCTGCAGATGAATCCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGCTGCTATTAGAACTAAGGTAC
ESTD- DRD2	--	--	--	---	---	TCTGCTTTGTGTCAGGAGGCTGCGGGGAGCCAGGAGCTGGAGATGGATGCTCTCCAGCAOCCA GCCCCCGAGAGGAGACCGGTACAGCCCCATCCACCCAGCCACACAGCTGACTCTCCCGACCCG TCCACACCGTCTCCACAGCACTCCCGACAGCCCGCCAAACAGAGAAATGGGCATGCCAAAG ACCAACCCAAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	--	---	---	AAGCAGTGGCCAGGATGAGCGCGCAGTAGGAGAGGECATAGTAGGCGATGTGGGGGGCCTGGCTGG CACCTGTGGATTCTGCCCCACAGGTGTAGTTAGGTGGCCACTCAGCTGCTCAGAGATGCCATA GCCCAGGGAGGTGCGTGATGCCAAGGGCTTCTCTGTGAGGAGA
ESTD- ERBB2	--	--	--	---	---	TCTTTCAGGATCCGCACTCTGCGCTGTGGGCTGCTCCGCTAGGTGTCAGCGGCTCCACCAGCTGG GGTGAGGGGTGTGGTCACTGTCGGGGGCGGTGCAGACCCACGCGGCTGGGAGGACTTCAACC CGCTCACCTCCGTTTCTGTCAGCAGTCTCCGCATCGTGTACT
ESTD- ETS2	--	--	--	---	---	ACTCACAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGGCACAGGAAGCCGCTCTGGGCTGGCA GTCCGTGGACGGGATGGTTCTGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTCTGGACACACAC AGACTATTTTAGATTTCTTTTGCCCTTTTGCAACCAAGAACAGCAAAATGCAAAAACCTCTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCTATTTCAGAAGTTAGTTG
ESTD-F2	--	--	--	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCACTGTGCAATGCAAGCTTAACCTCT GCACCAATGGCTCCAAAGCCCGTAGGGAACTGGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGCCGCTGCTGGTCCCAACAGAGAGGCGGTGGAGGAGGAGACAGGAGATGGGG TGGATGAG
ESTD-F9	--	--	--	---	---	AGATCCTGATGATTTTTTCTATTTTTTCTAATGTTTTACAGTTTGAAGTTTTAGATTTATGCCCA TGCTCCATTTTGAAGTTAATTTGTGTAAGTATGATGTTAAGTCAAACTTCATTTTTTTTTTCCATA GGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAC

ESTD- GODH	--	--	--	---	---	---	CGCAGACGGTCAGTGTGGGTGCGGAGTGTGGAGGGAAGGAGGAGGAAGAACTGGGGGTTTAGGGACT TTCCGGGTGACTTTCCCGTTCTGTGCTTCAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAAGGACCTCTGTGTCGACCGTGTGTTCTGCTGCCCTTTCAGCTGTCTGTCTGCGCGCAGTCGA CTCTGTCCCGGAAATTCGAGAGCT
ESTD-GOK	--	--	--	---	---	---	GTTTATGATGGCAGCTTAATGACAGGATGTCAGCCCTGCTGAGGCCACTCTGCTGTCACCATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCACCACCACTGGCTGG AGCAGGAAATGCGAGCGCGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCAAC TGCAGCCTAAITTACTCAAAGCTGTCCCGAGGTCACAG
ESTD- GNAT2	--	--	--	---	---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGTCAAACCCACAGGCATCATTG AAACCAAGTTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTCCCTAGG
ESTD- GPPK2L	--	--	--	---	---	---	AGTCTTCATCTGCGGTGCCAGGTAGATCCCTTCAOCCGCCGAGAACTGCTCGATATC
ESTD- HFRAS	--	--	--	---	---	---	CTGGGCTGCCCGCAGCAGCTGCTGCACTGAGCGGCGGCCAGGCTCAOCTCTATAGTGGGGTCG TATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	---	TTGGAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCCTGGGCCACATCTGGCCTTG AGGCCCTGCGAGGACCCCAAGAGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTCACCAAGCTATGATAACCTTAATTACACCTGAGCAAGAGTTCGGCCTCCGGCTTGATTCC AGATGGAGCTTCTCTTATCCCTGATGTATGGATTGGCTTCTCTGCTG
ESTD-HT2	--	--	--	---	---	---	GGGCTAAATTTCCGAGCACTTGCATAGACTGTTTATTGACTTGACAGGATGCTAGAGATAGG CAGGGAGAGGAAGATGTGTTACAGTTTGTGAGAGAGATAAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT4	--	--	--	---	---	---	ACCAGAGCCGGGATACAGACACTCTTAAGTTTGCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAAGTGGTCTTGGTGCTTCTATCGGCAAGATCGGTACTTATTTGAATAGTAGAGGTAA ACCACAGCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGCGGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	---	AACACAAAGCCCAAGGAGAAATTTGAAGTCCGACCCCTGGTTTACAAAGACAGTGTCTAACCCCT GAGCTATGAGCCCTGCTGCTGTGTTGTTTCTCTTCTTCATCTATAGATTGATGTTATGCTCTA GCATTCGGGTACCCGAATAGGATGTAGCTTGAGTAAATCCAGGATATTCTCTACAAAAATGAAA ACATTTCTGTGCTCTGTAAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	--	---	---	---	ACCCAGTGGAGCCCGCTCATTTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAAGGAAGATGTTT CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-8	--	--	--	--	TTTACTATTTCAATGGATACAGAAATTGTGGGAGTCACTATATTCCTATGAACAAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCTACATTTGTGAGTACGGGGCAGTGGTGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAATACTAATAACGGAGTTGAATATAAACCCCA
ESTD-IL1A	--	--	--	--	CAAAGTAAGCACCCCAATAATGTTAGCTATTACTATCATATTATTATTATTTATTTATTTTGG AGATGGAGTCTGGCTCTGTCACCCAGGCTGGAGTGCAGTGGCACATCTCGGCTCACTGCAAGCTCTG CCTCTGGGTTTCATGCCATCTCTGCTCAGCTCCGAGTAGTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAATTTTGTATTTTGTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	--	--	--	--	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCTCAGGAGCTCTCTGTCAATTGCAGG
ESTD- KRT10	--	--	--	--	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTAAAGTAACCTGCTAAGGTTTTTCCATTAAACCACCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	--	--	--	--	ACCTCACCCCTCCCTTAGCCCGTGGGAGCAGGAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCACGTCAACATTGACACA
ESTD- LF79	--	--	--	--	GGGTGATTTTGAGGCTCAGTTAATATTTCAAAATGTAAACCGTAGCAAACTGCATTGGTATTAGA AAAAATAAAATTTCCAATATGTAGTGTGTATTACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCGAGGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	--	TACACACTTTCTTACCCATTCACTGAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	--	TGTCAGTGTCCCTAGGGCACTCACCCTCCAGCTTCTCAGCTCTGCTGCTGCTGCTGCTGCA AGGGTTTGGCTTAATCTCAATCAATGCTCTTCACTCTTTTAGCAGCTGTGGGTTTTTGTGTTGTC TTCTGTTTGTCTAGTATCTGACTACTTTTAAATTATAAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTATTAAAAATTTTTCACCTG
ESTD-MCC	--	--	--	--	TTGTGAGGAGTGTGCTGCTGCTGCCCTCCAGCTCTGTCCCTAGCCGAACCTTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTGCTCTTCCAAGGGTTGGTCTAAGTTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTCTCTGTTTAGCATGG
ESTD-NF1	--	--	--	--	ATTATCCAGATGAATTTACAAAACCTATACCAGATCCCAAGACTGATATGGCTGGT

ESTD- NFKB1	--	--	--	---	---	---	---	---	---	AACATGGACTTGATATTGTACAAAAAAGTTTTATTTTCTAAAAAAGAAAAAGAAAA AAATTTAAAGGGTGTAATATATCCACACTGCACACTGCCTAGCCCAAAACGTCTTATTTGGTAGG ATCAGCCCTCATTTTGTGCTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTTGAAATTTCTGAG AAAACCTCTTTTAAACCTCACTTTGTGGGTTTTTGGAGAAGGTTATCA TGTCCTAGGCCAGCCCTGCTTGCTCCTCCCTGGCTGTATCTTCAGTACTGCAAGAGAACACACAGAC AT
ESTD- NPPA	--	--	--	---	---	---	---	---	---	GGAGGAGGAGGGGGAGGGGCTGCTGCTCCAGGTCACAGACCAGAGAGCGGCCTCAGTG TATCCCCACCCCAATGTGGCGCTGGAGATGAAGAGGAGTTGATGCAGGT
ESTD- NPAMP	--	--	--	---	---	---	---	---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTATGTAGGTGATATTGGATACCTTTTGTGTGATTATATAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTATGCTTATTTAACCTTGGCAATAGCATTTGC ATCCCTGTGGTTTTTAATAAAAT
ESTD- NPAS	--	--	--	---	---	---	---	---	---	GTGACCTTCTCACTTAAAAAATTTACCGGAGAAGAAATTAATATATGCTATGGCTATCAGCAGA TCTGAATTTAGGATAAACAGAAAGGAGGTATGTAACA
ESTD-OTC	--	--	--	---	---	---	---	---	---	GCCACCACCCACCCACAGCACACCTCCACCTCAGCCAGACAAGGTTGTACACAAGAGAGCCC TCAGGGCACAGAGAGATCTGGACACGTGGGAGTACCGGTGTATCATCGGAGGCGCGCGGCAC ATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTGGGCCCAAGTCTAGACAGACAAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAI1	--	--	--	---	---	---	---	---	---	CTCTTCAGGAACCCACAGTCTCTTACCAACACGACTTATTGCTGTCGAGAGGTACAAACCGTAGA ACTTCTCTCACTGTAATTTAGTTAAAGAAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTCACTTTCTGTGTTCTAGAACGTTTCTAG GACTGGCAGTTTAAGCTTTCACCTTAGGCTTTCTGTATACCCATGCCC
ESTD-PAR	--	--	--	---	---	---	---	---	---	CCTTCTCATGCCAGATGGAATTCAGTCCCTTCAGGATCTGCCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAAATCTTACCCGAGCTTGCTCGCATACAGACG GACAGTGTGTGGCAACATTGAAAGCCTCGTAAC
ESTD- PBDA	--	--	--	---	---	---	---	---	---	GGGAGTAAACTTGGATTGGAGATTTCATTTCTACAGTGTCTGGTGGTAAAGCCTCAGCAACA GCCAGTGAGACTGGAACACACCATAGCCTATTTCTGAGCCATATTAAATGGTTGTGCCCTACATT ATTACTCTTGCCATTTCAAGAAAGCATTGCCAGCTCTTCCAAATCTCCATCTCACCCTTTGGGCTTGT CTACTTTGCCACAGATTATCTTGTA
ESTD-PS-1	--	--	--	---	---	---	---	---	---	ATGAACATGGTCTTTAATTTATGATATGTTGTTATAGCTATCTTAAAGGGCTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAAGAGCGAGCTGTGGTGACAAAGTGTTTTTCTCAAGGCTCATACAGA TTCTGAAATCATGTGTCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTTATATCTT
ESTD- PXMP1	--	--	--	---	---	---	---	---	---	ACCTACAGACGTCGCTGGATGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG CTGGAGAAGAGCGTCCCGAGACTGGAAGGCT
ESTD- Per/RDS	--	--	--	---	---	---	---	---	---	

ESTD-PDS	--	--	--	---	---	---	CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGCTGGAGAAGAGCGTGCCGGAGACCTTGAAGG CCTTCTGAGAGTGTGAAGAGCTGGCAAGGCAACAGGTGGAAGCCGAGGGCGCAGACGCAGG CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC CCAAGAAACGTGGATCTCCCTCATCCAACCTCGAAAGTCTGAA
ESTD- RYR1	--	--	--	---	---	---	CTTGTGACGGGAGGTCACGTCTCCGCCCTCTTTCATGGACATATGGATGAGTGTGACCAATTTCCC CTGCTGACAGTGTATGACCAGCCAGACTTGTCTACTATGAGAGGGGAGCTGTGTGCACTCATGCCCGC TCCCTGAGGGCTGGAGCCACTGAGAATCAGCTGGAGTGGAGCCACCTGGCTGGGGCCAGCCACT CCGAGTCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	---	---	---	TGAACACCCTGTGTCGGAGCCAGGTGTGTTCTCTCTGGAGCCTGAGGAGTTTGTGTGTGTG CAGTCCCCCGCCACCTGCTGTTGAGCCTGGACATACACCTTCACCTCTTTGGCCCGGAGAAGAC ATTTACCCACTGGCCATGTCCCTGGCCTGTTGTGCACACCTCTGTGAAGACCCCAACCCCTGCTCC CCACCCCAAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	---	TTACATTTGTGGATTGTTCTTTTGTGCTGCGAGCACCTTTTCAACATGATGTATCCCATTTGTCCAAG TTTGTCTTGGCTGCTGTGCTGTGGGATATTGAAGAGATCTTTGCCAGTCCCAATGTCTAGAGAG TTTTCCCAATGTTTCTGTAAATAGTTTCATAGTTTGAGGCCCTAGATTTAAGTCTTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	--	--	--	---	---	---	AAATGGTCAGGACCCTGATCCACAAGAAGTGTGTTACCATTTTCATCAGGGCCCATCAGTTTCATCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAAGCTTGTTTACAACCTTTCTCCAGTATGGATGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THF8	--	--	--	---	---	---	TGCGCCCTTCTCTCGGCGAGGTAGACTTCTTACTTGGCTGTGTTTCCAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAACAGACACAGACCTGTGCCCAAAAGAAATGGAGG CAATAGGTTTGTAGGGGCATGAGGACGGGTTTCAGCCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAGACCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGTCCTCCAACTTTCCAAATCCCGCCCGCGGATGG
ESTD-TYR	--	--	--	---	---	---	TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGATTCTTGTTCACCCGCAACAGAGAGTCTATGC CAAGGCAGAAAGCTGTGCTTCATGGGCAAAATCAATGTCTCTCCAGATTTTCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGTCATCCAGACAAAGAGGTCAATAATTTGATGTGCTTAAACAT GGGTGTTGATCCATTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

ESTD- TYRP1	--	--	---	---	---	AGTAGGTGAAGCTAACAGCCTCTCTCACTGATCAGTATCAATGCTATGCTGAAGAATAGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCTATAGTATACAAA AACCACCTGGTTGAATATAATAGATTGAGTTAATTAAGTGTATTTCTTCACTTTATTAACCTTCTTTCT AATACAAGCATATGTTAGAATTAAAGTTCTAGGCATACTT
ESTD- VB12	--	--	---	---	---	TTCCCAAGGCGCTCAATACAAGTCTTTTCTTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACATGGAATGCTGGAATACCCAGAGCCCAAGACACAAGGTCAAGACAGAGAACACACAGTG ACTCTGAGATGTCACCACTGAGAACCCAGTATATGTAAGTGTATCGACAAGACCCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	--	---	---	---	AGGTAGGAAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGAACCTACCTTCCACACTGTCTTTGG TCCCTAGAGTCTG
ESTD-WT1	--	--	---	---	---	AAGACTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTGCTGCAGGATGTG CGACGTGTGCTGGAGTAGCCCGACTCTGTACGGTCGGCATCTGAGACCAGTGAAGAACGCCCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD- s14544	--	--	---	---	---	TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAGTTGAATGTCTCAGTTCGCTGTGTGGTTAGATGAGGATTTATATGATCCGTTAACCC TCT
EST71770 6	--	--	---	---	---	AGCACACCTCTCACGTCAAGCCTCAGCACAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGATACAGCTGTTGGTGAAGG AGTGCCAGTCCAGGCTGACACTGGACAAGAAAGAGGCCATCCAAAGG
EST52418 6	--	--	---	---	---	CAAATTACAGGTCAACTGCTATGATGTGTTGGAGCCAGTCACCCCTTTGGTGGCTACAAGATGTG GGGAGTGGCCGGGAGTTGGCGAGTACGGCTGCAGGCATACACTAAAGTGAAACTGTGAGTGTGG CCACTCTATTGCCAGCCCGGACAGAGCTGATCCTTGAACCTTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGCCAGGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAAGCAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTCGAGAGGAGGTGCTGCTGCTGCTGCCCCG GTCACTC
EST13586 3	--	--	---	---	---	AGGCAGAACTGGGCCCCCATCGGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAGGACCTGA GGGACAAAGGTCAACTCTCTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGAGGATGTCAGATGCTGGCC CCTTGGAGAGCTGAGCTGCCCTGGTGC
EST51976 7	--	--	---	---	---	

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EST11458 6						CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTCATCTTGTCTCGAGTTTT CTCTGCCATGTTGCTATTGACGACGGACCTGTCCAAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCAITAAAACATTCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTGTCC CGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8						CGGTCTTCTCCAGGTATTGTTGCAGAGCCGAGATGACCTCTATGTCTCAGATGCAATCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTACGGTACAGAAAGGAGATGCAATGAACAGCA GGAACACGTGGAAGGCCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAAT ACAGGCGT
EST62448 0						ACCTGGTGTGCTGTGGGTGAACCTGTGCTCTTGGCAITGCGGCGCTCTGCGGCGCGGTGG TCCTCTGTGTGCTGTGGGTAGTCTGTGGAGTCAACGGTCTCTTAGTGAAGCTGTGTGATGGCAACC CTGGAAACGATGGTCCCGAGGTGCGATGGTCAACCGGACACAAGGGAGAGCGCGGTTACCCCTGG CAATAT
EST38027 2						AGTGACTTCCAGGAAATGGCTACCCAACTTGGCTTCATGCGCTGTGGCCAACTATGCTCTCAGA ACATCACCTACCACCTGCAAGAACAGCATTGCATACATGATGAGGAGACTGGAACCTGAAAAAGG CTGTCACTTCTACAGGCTCTAATGATGTTGAACCTGTTGCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTGTAGATGGCTGCTCTAAAAGACAAATGAATGGGAAAGACAA
EST12274 0						CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTGCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAATATCTTCCCTCCTTAGGATGAGGTGA TAGTAAATGACCGATGGGTGAGAACTGTTCTGTCCATCCATGGAGGATACTATAACTGTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 7						ATGCTAAGGGGATCGGACATGAAGGAGCCCTGTGAGCCGATTGTCTCTATCTCCAGCGGCGCTGTCTATC CAGCTCACTCATCAATGGGCCAGTCAAGGCCAGGCACTGGGCTCCGAGGACTCACTGCCCCCT GCTGCCATGTGGACTGGTCAAGTTGAGGACTTCTTG
EST44438 7						GCAGCCAGGAGCGCTGCACCATGCCCCGATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGAGGTGGG
EST12839 3						TGCAAAACACACAAATCTTCCAGATGCGCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGG CCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACCTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCAGTTACTTATGAATATATGATACTTAGCTTAG
EST54419 8						CTTCTGCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCAGCTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTGGGTTAGCGTGGTCTGATGTTGCTCTACTA TAGTCCAAAGTGAA

EST10398 2						TGCTGGGTGGCAAGGCTGCAAAAGGAGGCAACCCAGGAGCTTTATGAAGCGGGCCATGGTA AGATGCTGCCAOCCTTATCTACTTGTGATGATGTTACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTGTTTCTTGGGCCAAGAGGTATCTACCAATAGTGTCTATTAGGCAITTG
EST36751 7						CCAAAGTCGTTCAATTTAGCTTTGCAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACCTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562						CACGTGGAAGGAGCTATTTTGAGGCTTTAAGAGTAAGAATCTGTCCCAAACTTTGTGGCTGAC TTTATGGCTAAGAAAGTTTCACTGATGATGATTAATAACAAATATTTACCTTTTGAAAAATAAATG AAGGATTGACCTGCTTCGCTCTGGAAGAGTATCGTACCGTCTGACGTTTGAACAATACAGAT GCCTTCCCTTGACAGTTTTCAGCCTCCTCTACCCCTA
EST18288 3						GCTCTCTATACCCCTGTGTCTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTGAGAA GATTGACAGGTTTCATGACGCTGTGACAGGATGGAAGACTGCTCTCCCTGACGGAGCCAGTGTGG ACAGCACCCCTGGCTTTCAACACCTACGTCCACTTCCAAAGGTAAAGCAAACTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3						TTCCGGCAGCCCCCATCTTGGCACCTTGGTCCCTCAGGGGCCACCCCGGGCACTCACCGCTCT CGCTCTCGGTAAACATCCGGCGCGCTCTTGACACATAGCTTGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGCTTGCAGGGGCCAGCCCTGCAGAGAGAGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
EST58707 7						CAGTGTATCTGGAAAGCCTACAGGACACCAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTACGATCTTTGGCTACATGAAGGCCAAATCCGAGAGACCCCTAGAAGATACACGAGACCGA ATGTATCAATGAGACATTCAGCAGGAATTCACGATACCTGTCTCTGGTAGGCCAGGTTTATAGCA CACTTGTACCTACATTTCTGATTGGTGGACTCTTGTCTAAGAACCTT
EST74167 6						AGACATGAAGGAGTTGAAGCCCTACAAATCGGAATGAGGAACAACCTGAACCCCGGTGGCGGAGG AGACGGGCAAGGCTGTCCAAAGGAGCTCAGGGCCGAGCCCGGCTGGCGCGGACATGAGGA CGTCGGCGCGCTGTGTCAGTACCGCGGAGGTGAGGCCATGCTGGCCAGAGCACCGGAGGAGC TGCGGGTGGCTGCTGCTCCACCTGGCAAGCTGGTAAGCGGCTCTC
EST43211 8						CGCTGTGTCAGTACCGCGGAGGTGACAGGCCATGCTGGCCAGAGCACCGAGGAGCTGGGGTGG CCTGCTCCACCTGGCAAGCTGCGTAAGCGGCTCTCCGATGCCGATGAOCTGCAGAAAGCGC TGGCAGTGTACAGGCGGGGCGCGAGGCGCGGAGCGGCTCAGGCGCATCGCGAGGCGGCTG GGGCGCTGTGGGAACAGGGCGCGTGGGGCGCCACTGTGGCTC
EST36770 4						TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGCAGCTATATCC ATCGAAATGTATTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCTCCGATAGGCTGGGCTGACCAAAATATAGTGGGTTTCTGTTTCTCTTCTGATCAT TCTTACAAGTTACTCTTATTGGAAAGGCCCTAAAGAGGCTTATG

EST26021 1	--	--	--	---	---	TAATGTAAAGCTCATCCACCAAGAAGCCTGCACCATTGTTTGAAGTTGAGTGACATGTTTCGAAACCTGT CCATAAAGTAATTTTGTGAAGAAGAGGAGCAAGAGAACATTCTCTGCAGCACTTCACGTACCAAAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGAGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTTTGCACAAGACAAAGCAAGCC
EST51212 0	--	--	--	---	---	ATCCTGAGCTCGCCAAATAAGCTTCTTGTTTCTACTTCTCTTCCACAAGCCCCAAATTTTCAGTTCTCA GAGGAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	--	--	--	---	---	GTCCGAATCCTCTCTGAAAGTGCCGGGTTTAACTCTGCTCATGCGCTGCGGCTGTGTCAGCT GAGGTGAGGGGCTTGAAGCTGGAGTGGGTTTAGGACGCGGCTCTGCGTGCACTCTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGAGTGGGTTTAGGACGCGGCTCTGCGTGCACTCTAAGCT CTGAGA
EST53018 6	--	--	--	---	---	ACAATCAGTGCACACATTCCAGAAGAGGAGGGTGTGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	--	---	---	CTTCTATGGGATTGACTTTATTTCTCCATTGTCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGAGCTCATGACAATTTGAAGCTGACAATTACACAAGAAGGAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTGAACCTTGTGTCACCTTTAATTACAACTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
EST34088 2	--	--	--	---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGCCACAAGAGACCGGCTCAAGG ATCCCAAGGCCCAACTCCCGAACCACTCAGGGTCTGTGTGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	--	---	---	CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCCACCCCTCTTTCTCTTCTCCCTTGA CTTTGAGTCAAAATGGCCTGACTTGAGTCCCTGAACCAAGCAAGAGAAAGAGAACCCAGAAAT CACAGGTGGGCACGTGCGCTACCGCCATCTCCCTCTCACGGGAATTTTCAGGGTAAACT
EST74082 --	--	--	--	---	---	TCCAGGGTGGCTGGACCCAGGCCCCAGCTCTGCAGCAGGAGGACGTGGCTCGTGAGGCATG TGGGGTGAGCCAGGGGCCCAAGGAGGCACTGGCTTCAGCTGCCCTCAGCCCTGCTGCTGTCAC CCAGATCACTGCTCTTGOCATGGCCCTGTGGATGCGCCTCTGCCCCCTGCTGGCGCTGCTGGCCCTC TGGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGCG
EST45311 0	--	--	--	---	---	GCCCTCCTCTCTTCCAAATCTGTCCCTATAGTTTCTCTATTAAAGTGAACATGCACTCTTTTAGT GGATAGATGCACAAACACACAAGCCATTATGGGAAGGATCCAGCTGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTCAATTTACAGCCCTTATTCATGGCCTTTTCTTTTCAGTAGTA CATACATCTGTGTCAATTTGTTGAAT

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining
comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.



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(21) International Application Number: PCT/US97/20313 (22) International Filing Date: 5 November 1997 (05.11.97) (30) Priority Data: 60/030,455 6 November 1996 (06.11.96) US (71) Applicant (for all designated States except US): WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Massachusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA). (74) Agents: GRANAHAH, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).	(81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 12 November 1998 (12.11.98)	
(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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INTERNATIONAL SEARCH REPORT

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According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 12607 A (MOLECULAR TOOL INC) 11 May 1995 see the whole document ---	1-20
X	WANG D ET AL: "TOWARD A THIRD GENERATION GENETIC MAP OF THE HUMAN GENOME BASED ON BI-ALLELIC POLYMORPHISMS" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 59, no. 4, October 1996, page A03 XP002050641 see abstract --- -/-	1-20

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *Z* document member of the same patent family

Date of the actual completion of the international search

17 June 1998

Date of mailing of the international search report

23. 09. 1998

Name and mailing address of the ISA

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Authorized officer

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INTERNATIONAL SEARCH REPORT

International Application No.

PC1/US 97/20313

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL10 emb1 Accession number: hst27766, 12 January 1995 ADAMS M D ET AL.: "Initial assessment of human gene diversity and expression patterns based upon 52 million basepairs of cDNA sequence" XP002067789 * Sequence *</p>	1-3,10,11
X	<p>SYVANEN A -CH ET AL: "IDENTIFICATION OF INDIVIDUALS BY ANALYSIS OF BIALLELIC DNA MARKERS,USING PCR AND SOLID-PHASE MINISEQUENCING" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 52, no. 1, January 1993, pages 46-59, XP002050638 see abstract see page 47, column 1, paragraph 3 - page 50, column 1, paragraph 1 see page 51, column 1, paragraph 3; figure 1; table 1</p>	1-3,7-10,13,14,17-20
X	<p>FR 2 722 295 A (ROUSSY INST GUSTAVE) 12 January 1996 see abstract see page 1, line 5 - page 2, line 17 see page 9, line 9 - page 10, line 15; tables 2,3</p>	1-3,7-9,17-20
X	<p>HRUBAN R H ET AL: "K-RAS ONCOGENE ACTIVATION IN ADENOCARCINOMA OF THE HUMAN PANCREAS A STUDY OF 82 CARCINOMAS USING A COMBINATION OF MUTANT-ENRICHED POLYMERASE CHAIN REACTION ANALYSIS AND ALLELE-SPECIFIC OLIGONUCLEOTIDE HYBRIDIZATION" AMERICAN JOURNAL OF PATHOLOGY, vol. 143, no. 2, 1 August 1993, pages 545-554, XP000572114 see the whole document</p>	10-16,18-20
X	<p>GROMPE M: "THE RAPID DETECTION OF UNKNOWN MUTATIONS IN NUCLEIC ACIDS" NATURE GENETICS, vol. 5, no. 2, October 1993, pages 111-117, XP000615290 see the whole document</p>	18-20

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INTERNATIONAL SEARCH REPORT

International Application No

PC1/US 97/20313

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>NIKIFOROV T T ET AL: "GENETIC BIT ANALYSIS: A SOLID PHASE METHOD FOR TYPING SINGLE NUCLEOTIDE POLYMORPHISMS" NUCLEIC ACIDS RESEARCH, vol. 22, no. 20, October 1994, pages 4167-4175, XP002015765 see the whole document</p> <p style="text-align: center;">-----</p>	18-20

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 97/20313

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-20 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-20 (partially)

INVENTION 1: An isolated nucleic acid segment including a polymorphic site having the nucleotide sequence of SEQ ID NO:1149, or the complement of that segment or portions thereof, an allele-specific oligonucleotide probe or primer hybridizing to such a segment or its complement, and a method of analyzing such a nucleic acid by determining the bases occupying the polymorphic site(s).

2. Claims: 1-20 (partially)

INVENTION 2 to INVENTION 2669:

-Idem as invention 1 but limited to the sequences having SEQ ID Nos. 1150 to 3817. (Invention 2 is limited to SEQ ID NO:1150, invention 3 is limited to SEQ ID NO:1151, ..., invention 2669 is limited to SEQ ID NO:3817).

For the sake of conciseness, the first group is explicitly defined, the other groups are defined by analogy hereto.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PC, /US 97/20313

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9512607 A	11-05-95	AU 8132194 A	23-05-95
		CA 2175695 A	11-05-95
		EP 0726905 A	21-08-96
		US 5762876 A	09-06-98

FR 2722295 A	12-01-96	NONE	
